

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 90.0757 Seconds  
(without alignments)  
2239.886 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFYLL.....STGLHSLSTFRLMKRRSV 394

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2042	100.0	394	1 CIW3 HUMAN	O14649 homo sapien
2	1850.5	90.6	411	1 CIW3 RAT	O54912 rattus norv
3	1840.5	90.1	409	1 CIW3 MOUSE	O35111 mus musculus
4	1732	84.8	392	2 Q9ESM5	Q9ESM5 rattus norv
5	1333	65.3	299	2 Q9QX34	Q9QX34 mus musculus
6	1298.5	63.6	301	2 Q9ESM4	Q9ESM4 rattus norv
7	1150	56.3	374	2 Q63Z10	Q63Z10 xenopus lae
8	1116	54.7	374	1 CIW9 HUMAN	Q9NPC2 homo sapien
9	1069.5	52.4	365	1 CIW9 CAVPO	Q9J158 cavia porce
10	999	48.9	396	2 Q923V6	Q923V6 rattus norv
11	960.5	47.0	395	2 Q9JLD4	Q9JLD4 rattus norv
12	924	45.2	237	1 CIW9 RAT	Q9ES08 rattus norv
13	916.5	44.9	318	1 CIWF RAT	Q9H427 homo sapien
14	846	41.4	330	1 CIWF HUMAN	Q9H427 homo sapien
15	820	40.2	329	2 O17185	O17185 caenorhabdi
16	777	38.1	340	2 Q9VHE0	Q9VHE0 drosophila
17	769	37.7	307	2 Q7PZH9	Q7PZH9 anopheles g
18	760.5	37.2	345	2 Q7QC61	Q7QC61 anopheles g
19	742	36.3	398	2 Q9VFS9	Q9VFS9 drosophila
20	732.5	35.9	370	2 Q9JL57	Q9JL57 cavia porce
21	599	29.3	364	2 Q9L790	Q9L790 caenorhabdi
22	558.5	27.4	121	2 Q867A3	Q867A3 oryctolagus
23	373	18.3	405	1 CIW2 MOUSE	Q8R1P5 mus musculus
24	370	18.1	411	1 CIW2 MOUSE	P97438 mus musculus
25	369	18.1	405	1 CIW2 RAT	Q9ES08 rattus norv
26	367	18.0	426	2 Q920B6	Q920B6 rattus norv
27	366	17.9	414	2 Q6P6P9	Q6P6P9 mus musculus
28	364	17.8	426	1 CIW2 HUMAN	Q9S069 homo sapien
29	363	17.8	411	2 Q9NR72	Q9NR72 homo sapien
30	361	17.7	309	1 CIW2 HUMAN	Q9C555 homo sapien
31	360	17.6	411	2 Q8HY88	Q8HY88 bos taurus

32	358.5	17.6	331	2 Q8AVIS	Q8AVIS xenopus lae
33	358	17.5	408	1 CIWD HUMAN	Q9H614 homo sapien
34	354	17.3	294	2 Q6X6Z5	Q6X6Z5 homo sapien
35	349.5	17.1	453	2 Q8BZB0	Q8BZB0 m mus muscu
36	349.5	17.1	535	2 Q8BUW1	Q8BUW1 m mus muscu
37	349.5	17.1	538	1 CIWA HUMAN	P57789 homo sapien
38	349.5	17.1	538	1 CIWA RAT	Q9J184 rattus norv
39	349.5	17.1	538	2 Q6Q834	Q6Q834 oryctolagus
40	349.5	17.1	543	2 Q6B014	Q6B014 homo sapien
41	346.5	17.0	262	2 Q6X6Z3	Q6X6Z3 homo sapien
42	345.5	16.9	426	2 Q8I6M6	Q8I6M6 aplysia cal
43	341	16.7	323	2 Q6PEI1	Q6PEI1 brachydanio
44	334.5	16.4	322	2 Q6X6Z4	Q6X6Z4 homo sapien
45	334	16.4	307	2 Q801T4	Q801T4 xenopus lae

#### ALIGNMENTS

RESULT 1  
ID CIW3 HUMAN STANDARD; PRT; 394 AA.  
AC O14649;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1) (Two pore potassium channel KT3.1).  
DE Name=KCNK3; Synonyms=TASK, TASK1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464; Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations near physiological pH.";  
RL EMBO J. 16:5464-5471(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.N.; "proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP ACTIVATION.  
RX MEDLINE=99254548; PubMed=1031245; DOI=10.1038/8084; Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.; "Inhalational anesthetics activate two-pore-domain background K+ channels.";  
RL Nat. Neurosci. 2:422-426(1999).  
RN [4]  
RP MUTAGENESIS OF HIS-98.  
RX MEDLINE=21535313; PubMed=11680614; Ashmole I., Goodwin P.A., Stanfield P.R.; "TASK-5, a novel member of the tandem pore K+ channel family.";  
RL Pflügers Arch. 442:828-833(2001).  
CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Widespread expression in adult. Strongest expression in pancreas and placenta. Lower expression in brain, lung, prostate, heart, kidney, uterus, small intestine and colon.  
CC -!- MISCELLANEOUS: Inhibited by external acidification. Activated by

halothane and isoflurane.  
 -!- SIMILARITY: belongs to the two pore domain potassium channel  
 (TC 1.A.1.8) family.

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
 EMBL; AF006823; AAC51777.1; -;  
 EMBL; AF065163; AAG29340.1; -;  
 GenBank; HGNC:6278; KCNK3.  
 MIM; 603220; -;  
 GO; GO:0005887; C:integral to plasma membrane; TAS.  
 GO; GO:0005267; F:potassium channel activity; TAS.  
 GO; GO:0006813; P:potassium ion transport; TAS.  
 GO; GO:0007268; P:synaptic transmission; TAS.  
 InterPro; IPR005821; Ion trans.  
 InterPro; IPR003280; K-channel\_2pore.  
 InterPro; IPR001622; K-channel\_pore.  
 InterPro; IPR005406; TASK1 channel.  
 InterPro; IPR003092; TASK channel.  
 Pfam; PF00520; Ion trans\_1.  
 PRINTS; PR01333; 2PORECHANNEL.  
 PRINTS; PR01584; TASK1CHANNEL.  
 KW Glycoprotein; Ion transport; Ionic channel; Potassium;  
 Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 FT DOMAIN 1 8 Cytoplasmic (Potential).  
 FT TRANSMEM 9 29 Potential.  
 FT DOMAIN 78 101 Pore-forming 1 (Potential).  
 FT TRANSMEM 108 128 Potential.  
 FT DOMAIN 129 158 Cytoplasmic (Potential).  
 FT TRANSMEM 159 179 Potential.  
 FT DOMAIN 184 207 Pore-forming 2 (Potential).  
 FT TRANSMEM 223 243 Potential.  
 FT DOMAIN 244 394 Cytoplasmic (Potential).  
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).  
 FT MUTAGEN 98 98 H->N: Greatly reduces pH sensitivity.  
 SQ SEQUENCE 394 AA; 43518 MW; 9FF4C8266F615FB7 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-153;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQVRLALIVCTFTYLLVGAAPDALESEPELIERQRLRQELRARNYLSQGGYE 60  
 DB 1 MKRQVRLALIVCTFTYLLVGAAPDALESEPELIERQRLRQELRARNYLSQGGYE 60

QY 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDGKVFCEYALLGIPL 120  
 DB 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDGKVFCEYALLGIPL 120

QY 121 TLVVFQSLGERINTLVRYLLHRAKGLGNRRADVSNMNVLIQFFSCITLCIGAAAFSH 180  
 DB 121 TLVVFQSLGERINTLVRYLLHRAKGLGNRRADVSNMNVLIQFFSCITLCIGAAAFSH 180

QY 181 YEHWTFFQAYYCFITLTITIGDYVALQDQALQTPQYVAFSFVYILTLGTIVTIGAFIN 240  
 DB 181 YEHWTFFQAYYCFITLTITIGDYVALQDQALQTPQYVAFSFVYILTLGTIVTIGAFIN 240

QY 241 LVVLRFTMTNABDEKDAEHRALLTRNGAGGGGGGSAHTTDTTASSTAAAGGGFRNYY 300  
 DB 241 LVVLRFTMTNABDEKDAEHRALLTRNGAGGGGGGSAHTTDTTASSTAAAGGGFRNYY 300

QY 301 AEVLHFQSCSLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGYSTPSSR 360  
 DB 301 AEVLHFQSCSLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGYSTPSSR 360

QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

-----  
 RESULT 2  
 ID CIW3 RAT STANDARD; PRT; 411 AA.  
 AC O54912;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)  
 DE (Two pore potassium channel KT3.1).  
 DE Name=Kcnk3; Synonyms=Taek, Task1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID=10116;  
 RX [1]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Cerebellum;  
 RX MEDLINE=98099797; PubMed=9437008;  
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;  
 RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum";  
 RL J. Neurosci. 18:868-877(1998).  
 CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Strongest expression in heart. Moderate expression in lung and brain. Low levels in liver, kidney and skeletal muscle.  
 CC -!- MISCELLANEOUS: Inhibited by extracellular acidification, zinc, bupivacaine and phenytoin. Activated by protein kinase A.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
 EMBL; AF031384; AAC39952.1; -;  
 RGD; 61997; Kcnk3.  
 InterPro; IPR005821; Ion trans.  
 InterPro; IPR003280; K-channel\_2pore.  
 InterPro; IPR001622; K-channel\_pore.  
 InterPro; IPR005406; TASK1 channel.  
 InterPro; IPR003092; TASK channel.  
 Pfam; PF00520; Ion trans\_1.  
 PRINTS; PR01333; 2PORECHANNEL.  
 PRINTS; PR01584; TASK1CHANNEL.  
 KW Glycoprotein; Ion transport; Ionic channel; Potassium;  
 Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 FT DOMAIN 1 8 Cytoplasmic (Potential).  
 FT TRANSMEM 9 29 Potential.  
 FT DOMAIN 78 101 Pore-forming 1 (Potential).  
 FT TRANSMEM 108 128 Potential.  
 FT DOMAIN 129 158 Cytoplasmic (Potential).  
 FT TRANSMEM 159 179 Potential.  
 FT DOMAIN 184 207 Pore-forming 2 (Potential).  
 FT TRANSMEM 223 243 Potential.  
 FT DOMAIN 244 411 Cytoplasmic (Potential).

```

FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 411 AA; 45276 MW; D2778016B092E2BF5 CRC64;

Query Match
Best Local Similarity 88.3%; Score 1850.5; DB 1; Length 411;
Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;

QY 1 MKQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
DB 1 MKQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
QY 61 ELERVVRLKPKHAGVQWRFAAGFYFAITVITIGYCHAAPSTDGKVKFCMFALLGIPL 120
DB 61 ELERVVRLKPKHAGVQWRFAAGFYFAITVITIGYCHAAPSTDGKVKFCMFALLGIPL 120
QY 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
DB 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
QY 181 YEHWTFFQAYYYCFITLTIGFGDYVALQDQALQTOQPVAFSVFVILTGLTVIGAFLN 240
DB 181 YERWTFQAYYYCFITLTIGFGDYVALQDQALQTOQPVAFSVFVILTGLTVIGAFLN 240
QY 241 LVVLRFTWNAEKRDAEHRALLTRNGQAGGGG-----GGSAAHTTDTASATAA- 291
DB 241 LVVLRFTWNAEKRDAEHRALLTRNGQAGGGG-----GGSAAHTTDTASATAA- 291
QY 292 -----GGGGRNRYAEVHLFQSCSLWYKREKLOYISPMIIPRDLSTSDTCTVEOS 343
DB 292 -----GGGGRNRYAEVHLFQSCSLWYKREKLOYISPMIIPRDLSTSDTCTVEOS 343
QY 301 GMGVGVGVGGSGFRNRYAEMHLFQSCSLWYKREKLOYISPMIIPRDLSTSDTCTVEOS 360
DB 301 GMGVGVGVGGSGFRNRYAEMHLFQSCSLWYKREKLOYISPMIIPRDLSTSDTCTVEOS 360
QY 344 HSPGPGGGYSDTPSRRLCSGAPRAISVSTGLHSLSTFRLGMLKRRSSV 394
DB 361 HSPGPGGGYSDTPSPCLCSGTORSAISSVSTGLHSLSTFRLGMLKRRSSV 411

RESULT 3
CIW3_MOUSE
ID ID CIW3_MOUSE STANDARD; PRT; 409 AA.
AC O3511; O35163;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE (Cardiac two-pore background K+ channel) (cTBK-1) (Two pore potassium
DE channel KT3.1).
GN Name-Kcnk3; Synonyms=CtbaK, TASK, Task1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98165556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurachi Y.;
RT "Cloning and functional expression of a novel cardiac two-pore
RT background K+ channel (cTBK-1).";
RL Circ. Res. 82:513-518 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=20287574; PubMed=10748056; DOI=10.1074/jbc.M001948200;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the
RT cardiac leak channel Kcnk3.";
RL J. Biol. Chem. 275:16969-16978 (2000).
RN [3]
RP SEQUENCE OF 4-409 FROM N.A.
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations

```

```

RT near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
CC -I- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein. Rectification direction results from potassium
CC ion concentration on either side of the membrane. Acts as an
CC outward rectifier when external potassium concentration is low.
CC When external potassium concentration is high, current is inward
CC (by similarity).
CC -I- SUBUNIT: Homodimer (Potential).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Very strong expression in heart, also detected
CC in kidney, brain, skin, testis, lung, skeletal muscle, small
CC intestine and stomach. Not detected in liver, thymus or spleen.
CC -I- MISCELLANEOUS: Inactivated by barium.
CC -I- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB008537; BAA25436.1; -
CC EMBL; AF241798; AAF81418.1; -
CC EMBL; AF242508; AAF81418.1; JOINED.
CC EMBL; AF065162; AAG29339.1; -
CC EMBL; AF006824; AAC53367.1; -
CC EMBL; AB013345; BAA28349.1; -
CC MGD; MGI:1100509; Kcnk3.
CC InterPro: IPR005821; Ion trans.
CC InterPro: IPR003280; K+channel_2pore.
CC InterPro: IPR001622; K+channel_pore.
CC InterPro: IPR005406; TASK1_channel.
CC InterPro: IPR003092; TASK_channel.
CC Pfam; PF00520; Ion trans; 1.
CC PRINTS; PR01333; 2POREKCHANEL.
CC PRINTS; PR01584; TASK1CHANNEL.
CC PRINTS; PR01095; TASKCHANNEL.
CC Glycoprotein; Ion transport; Ionic channel; Potassium;
CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
CC FT DOMAIN 1 8 Cytoplasmic (Potential).
CC TRANSMEM 9 29 Pore-forming 1 (Potential).
CC FT DOMAIN 78 101 Potential.
CC TRANSMEM 108 128 Cytoplasmic (Potential).
CC FT DOMAIN 129 158 Potential.
CC TRANSMEM 159 179 Pore-forming 2 (Potential).
CC FT DOMAIN 184 207 Potential.
CC TRANSMEM 223 243 Cytoplasmic (Potential).
CC FT DOMAIN 244 409 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 53 53 Q -> E (in Ref. 3).
CC FT CONFLICT 4 4 V -> I (in Ref. 3).
CC FT CONFLICT 123 123 SEQUENCE 409 AA; 45068 MW; 35236E011AAC5687 CRC64;
SQ SEQUENCE 409 AA; 45068 MW; 35236E011AAC5687 CRC64;

Query Match
Best Local Similarity 88.5%; Score 1840.5; DB 1; Length 409;
Matches 362; Conservative 7; Mismatches 25; Indels 15; Gaps 2;

QY 1 MKQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
DB 1 MKQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
QY 61 ELERVVRLKPKHAGVQWRFAAGFYFAITVITIGYCHAAPSTDGKVKFCMFALLGIPL 120
DB 61 ELERVVRLKPKHAGVQWRFAAGFYFAITVITIGYCHAAPSTDGKVKFCMFALLGIPL 120
QY 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
DB 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180

```

```

QY 181 YEHWTFFOAYYYCFITLTTIGFDYVALQKQALQTOPOYVAFSFVYILTLGLTVIGAFIN 240
|||
Db 181 YERWTFFOAYYYCFITLTTIGFDYVALQKQALQTOPOYVAFSFVYILTLGLTVIGAFIN 240
|||
QY 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTTASSTAAA- 291
|||
Db 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTTASSTAAA- 291
|||
QY 292 -----GGGGRNVVAEVLHFQSMCCLWYKREKLOYISIPMIIPRDLSTSDTCVESH 345
|||
Db 292 -----GGGGRNVVAEVLHFQSMCCLWYKREKLOYISIPMIIPRDLSTSDTCVESH 345
|||
QY 301 GVGVGVGSGGRNVVAEVLHFQSMCCLWYKREKLOYISIPMIIPRDLSTSDTCVESH 360
|||
Db 301 GVGVGVGSGGRNVVAEVLHFQSMCCLWYKREKLOYISIPMIIPRDLSTSDTCVESH 360
|||
QY 346 SPGGGGRYSDTSPRRCLCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 394
|||
Db 346 SPGGGGRYSDTSPRRCLCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 394
|||
QY 361 SPGGGGRYSDTSPRRCLCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 409
|||

RESULT 4
Q9ESM5 PRELIMINARY; PRT; 392 AA.
AC Q9ESM5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE TASK1 splice bvariant (TASK1b).
GN Name-KCNK3b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ohya S., Kitsukawa M., Imaizumi Y.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
(CC 1.A.1.8) family.
DR EMBL; AB048823; BAB16710.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005406; TASK1 channel.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FOREKCHANNEL.
DR PRINTS; PR01584; TASK1CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 392 AA; 43150 MW; F5438B12AAD7FB1B CRC64;

Query Match 84.8%; Score 1732; DB 2; Length 392;
Best Local Similarity 83.9%; Pred. No. 4.8e-129;
Matches 345; Conservative 7; Mismatches 23; Indels 36; Gaps 4;

QY 1 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSSGGYE 60
|||
Db 1 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSSGGYE 60
|||
QY 61 ELERVRLKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPL 120
|||
Db 42 ELERVRLKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPL 101
|||
QY 121 TLVFMFOSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSH 180
|||
Db 102 TLVFMFOSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSY 161
|||
QY 181 YEHWTFFOAYYYCFITLTTIGFDYVALQKQALQTOPOYVAFSFVYILTLGLTVIGAFIN 240
|||

```

## RESULT 5

```

Q9QX34 PRELIMINARY; PRT; 299 AA.
AC Q9QX34;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative potassium channel DP4 (Fragment).
GN Name-Kcnk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
(CC 1.A.1.8) family.
DR EMBL; AF022821; AAD09338.1; -.
DR MGD; MGI:1100509; Kcnk3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005406; TASK1 channel.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FOREKCHANNEL.
DR PRINTS; PR01584; TASK1CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 299
SQ SEQUENCE 299 AA; 33325 MW; DCD41D8A212939C4 CRC64;

Query Match 65.3%; Score 1333; DB 2; Length 299;
Best Local Similarity 88.9%; Pred. No. 1.6e-97;
Matches 263; Conservative 7; Mismatches 18; Indels 8; Gaps 1;

QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSSGGYE 63
|||
Db 2 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSSGGYE 61
|||
QY 64 RVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPLTV 123
|||
Db 62 RVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPLTV 121
|||
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSHYBH 183
|||
Db 122 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSYER 181
|||
QY 184 WFFFQAYYYCFITLTTIGFDYVALQKQALQTOPOYVAFSFVYILTLGLTVIGAFINLVV 243
|||
Db 182 WFFFQAYYYCFITLTTIGFDYVALQKQALQTOPOYVAFSFVYILTLGLTVIGAFINLVV 241
|||

```



QY 244 LRPMWNAEDKDAEHRALLTNGQAGGGG-----GCSAHTTDTASSTAAA 291  
 |||||  
 Db 242 LRPMWNAEDKDAEHRALLTNGQAVGLGSLGSLGVRPRDPVTCAAA 297  
 |||||

RESULT 6  
 Q9ESM4  
 ID Q9ESM4 PRELIMINARY; PRT; 301 AA.  
 AC Q9ESM4  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE TWIK-related acid-sensitive K<sup>+</sup> channel splice variant (TASK1c).  
 GN Name=KCNK3c;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RA Ohya S., Kitsuikawa M., Imaizumi Y.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL: AB048824; BAB16711.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR001623; K+channel pore.  
 DR InterPro; IPR005406; TASK1\_channel.  
 DR InterPro; IPR003092; TASK\_channel.  
 DR PRINTS; PRO1584; TASK1CHANNEL.  
 DR PRINTS; PRO1095; TASKCHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 301 AA; 32811 MW; 265DE38DFA79595E CRC64;

Query Match 63.8%; Score 1298.5; DB 2; Length 301;  
 Best Local Similarity 85.0%; Pred. No. 8.6e-95;  
 Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2;

QY 111 MFVALGIPLTLMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLGFFSCIST 170  
 |||||  
 Db 1 MFVALGIPLTLMFQSLGERINTFVRYLLHRAKGLGMRHADVSMANMVLGFFVSCIST 60  
 |||||

QY 171 LCIGAAAFSHYEHWTFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYVILT 230  
 |||||  
 Db 61 LCIGAAAFSYERWTFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYVILT 120  
 |||||

QY 231 GLTVIGAFNLVLRPMTWNAEDKDAEHRALLTNGQAGGGG-----GCSAHTT 282  
 |||||  
 Db 121 GLTVIGAFNLVLRPMTWNAEDKDAEHRALLTNGQAGGIGLGLSCLSGSLGCVRP 180  
 |||||

QY 283 DTASSTAAA-----GGGGRNNYAEVLHFSQSMCCLWYKREKLOYSTPMIIPDL 333  
 : : : : :  
 Db 181 DPVTCAAAAGMGVGVGVGSGGRNNYAEMLHFSQSMCCLWYKREKLOYSTPMIIPDL 240  
 : : : : :  
 QY 334 STSDTCEVSHSSPGGGGRYSDTPSRCLCSGAPRAISSVSTGLSHLSLTFGLMKRRSS 393  
 |||||  
 Db 241 STSDTCEVSHSSPGGGGRYSDTPSPHCLCSGTQRSRAISSVSTGLSHLSLTFGLMKRRSS 300  
 |||||

QY 394 V 394  
 |  
 Db 301 V 301

RESULT 7  
 Q63Z10  
 ID Q63Z10 PRELIMINARY; PRT; 374 AA.  
 AC Q63Z10  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603099;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC082937; AAH82937.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 374 AA; 42718 MW; 8F37D8FF1F689F63 CRC64;

Query Match 56.3%; Score 1150; DB 2; Length 374;  
 Best Local Similarity 59.6%; Pred. No. 6.6e-83;  
 Matches 235; Conservative 47; Mismatches 92; Indels 20; Gaps 4;

QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELRQCELARVNLSSGGYE 60  
 : : : : :  
 Db 1 MKRQNVRLSLICITFTYLLVGAAVFDALSEYEWREKLEKAEIRLKGKYNISSEYR 60  
 : : : : :  
 QY 61 ELERVVLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDGKVKFCMFYALIGIPL 130  
 : : : : :  
 Db 61 QLELVIMQSEPHRAGVQWKFGSFYFAITVITIGYHAAPSTDGKVKFCMFYALIGIPL 120  
 : : : : :  
 QY 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLGFFSCISTLCIGAAAFSH 180  
 |||||  
 Db 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLGFFSCISTLCIGAAAFSH 180  
 |||||

QY 181 YEHWTFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYVILTLTVIGAFNL 240  
 |||||  
 Db 181 YEEMFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYVILTLTVIGAFNL 240  
 |||||

QY 241 LVVLRFMWNAEDKDAEHRALLTNGQAGGGGSAHTTDTASSTAAAGGGGPRNVY 300  
 |||||  
 Db 241 LVVLRFLTWNSDERRDAEERASL-----AGNRNSMIITHIQEDTPH-----GRQRYK 287  
 : : : : :  
 QY 301 AEVLHFSQSMCCLWYKREKLOYSTPMIIPDLSTSDTCEVSHSSPGGGGRYSDTPSR 360  
 |||||

Db 288 ABVTLQSVSCMCYRSHE---YTRSMVSHQNSFSSKLNQVYFHSISYKIBEISPTLKN 344

Qy 361 CLCSGAPRSATSSVSTGLHSLSTFGLMKRRSSV 394

Db 345 SLFP-----SPVSSVSGFLHSLFTDKHRLMKRRKSI 374

RESULT 8

CIW9 HUMAN STANDARD; PRT; 374 AA.

AC Q9NFC2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3)

DE (Two pore potassium channel KT3.2).

DE Name=KCNK9; Synonyms=TASK3;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20287530; PubMed=10747866; DOI=10.1074/jbc.M000030200;

RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Derst C.,

RA "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor";

RT J. Biol. Chem. 275:16650-16657 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Cerebellum.

RX PubMed=11042359; DOI=10.1016/S0169-328X(00)00183-2;

RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kellell R.E., Murdoch P.R., Randall A.D., Rennie G.I., Gloger I.S.;

RT "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel";

RL Brain Res. Mol. Brain Res. 82:74-83 (2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Girard C., Lesage F., Tinel N., Lazdunski M.;

RT "Human Task-3, a novel 2p domain potassium channel related to Task.1";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=21324619; PubMed=11431495;

RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D., Coetzee W.A., Rudy B.;

RA "KT3.2 and KT3.3, two novel human two-pore K(+) channels closely related to TASK-1";

RT J. Neurophysiol. 86:130-142 (2001).

RL -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Mainly found in the cerebellum. Also found in adrenal gland, kidney and lung.

CC -!- MISCELLANEOUS: Inhibited by phorbol 12-myristate 13-acetate (PMA). Insensitive to changes in the pH range of 7-8.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; AF212829; AAF63708.1; -.

DR EMBL; AF248241; AAG31730.1; -.

DR EMBL; AF279809; AAF85982.1; -.

DR EMBL; AF257080; AAG33126.1; -.

DR Genew; HGNC:6283; KCNK9.

DR MIM; 605874; -.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0005267; P:potassium channel activity; NAS.

DR GO; GO:0006813; P:potassium ion transport; NAS.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR003280; K+channel 2pore.

DR InterPro; IPR001622; K+channel\_pore.

DR InterPro; IPR005407; TASK3 channel.

DR InterPro; IPR003092; TASK3 channel.

DR Pfam; PF00520; Ion trans; 1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01585; TASK3CHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

KW Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.

KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.

FT DOMAIN 1 8 Cytoplasmic (Potential).

FT TRANSMEM 9 29 Potential.

FT DOMAIN 78 101 Pore-forming 1 (Potential).

FT TRANSMEM 108 128 Potential.

FT DOMAIN 129 158 Cytoplasmic (Potential).

FT TRANSMEM 159 179 Potential.

FT DOMAIN 184 207 Pore-forming 2 (Potential).

FT TRANSMEM 219 239 Potential.

FT DOMAIN 240 374 Cytoplasmic (Potential).

FT CARBOHYD 53 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 374 AA; 42263 MW; 8A19AE5EA4D7F38 CRC64;

Query Match 54.7%; Score 1116; DB 1; Length 374;

Best Local Similarity 59.0%; Pred. No. 3.3e-80;

Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Qy 1 MKRQVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARVNLGGVE 60

Db 1 MKRQVRLSLIVCTFTYLLVGAADFDALESDHEEKEKAEIRIKGTNISEDYR 60

Qy 61 ELERVVLRLKPKAGVQWRVAGSFYFAITVTTTIGYGHAAAPSTGGKVFYALLGIPL 120

Db 61 QLELVILQSEPHRAGVQWKFAGSFYFAITVTTTIGYGHAAAPCTDAGKAFYAVLGIPL 120

Qy 121 TLVNFQSLGERINTLVRLHRAKGLQWRADVSMANVLIGFPSCSTLCIGAAAFSH 180

Db 121 TLVNFQSLGERMNTFVRLKRIKKCCQMRNTVSMENNVTGVFFSCMTLCIGAAAFSQ 180

Qy 181 YEHWTFFQAYYCYTTLTIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAFLN 240

Db 181 CEESWFFHAYYCYTTLTIGFDYVALQDQALQKPLLYVAFSPYILVGLTVIGAFLN 240

Qy 241 LVVLRFTMTNAEDEKRAEHRALLTRNQAGGGGGGSAHTTDTASTAAAGGGGFRNYY 300

Db 241 LVVLRFTMTNSEDERDAEERASL-----AGNRNSMWIHIPEERPS-----RPRY 286

Qy 301 -AEVLHFQSCSLWYKREKLQYISPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTFSR 359

Db 287 KADVPDLQSVCSCTCYRSQD---YGRSVAPQNSFSAKLAPHYFHSISYKIBEISPTLTK 343

Qy 360 RCLCSGAPRSATSSVSTGLHSLSTFGLMKRRSSV 394

Db 344 NSLFP-----SPVSSVSGFLHSLFTDKHRLMKRRKSV 374

RESULT 9

CIW9 CAVPO STANDARD; PRT; 365 AA.

ID Q9JUL58;

AC Q9JUL58;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).

DE Name=KCNK9; Synonyms=TASK3;

GN Cavia porcellus (Guinea pig).



```
ID Q9JLD4 PRELIMINARY; PRT; 395 AA.
AC Q9JLD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
RA Coetzee W.A., Rudy B.;
RT "Kt3.2 and kt3.3, two novel human two-pore k(+) channels closely
RT related to TASK-1.";
RL J. Neurophysiol. 86:130-142(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Kim Y., Bang H.W., Kim D.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBSJ databases.
CC -! SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
DR EMBL; AF192366; AAF60229.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005407; TASK3_channel.
DR InterPro; IPR003092; TASK3_channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2POREKCHANEL.
DR PRINTS; PR01585; TASK3CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
DR Ion transport; Ionic channel; Transmembrane; Transport.
DR SEQUENCE 395 AA; 44365 MW; 3F76F7923A3AFC76 CRC64;

Query Match 47.0%; Score 960.5; DB 2; Length 395;
Best Local Similarity 69.7%; Pred. No. 7.6e-68;
Matches 186; Conservative 31; Mismatches 49; Indels 1; Gaps 1;

QY 1 MKRQVRLALVCTFTLLVGAAPFDALSEPELIERQRLROELRARNYLNLSGGYE 60
Db 1 MKRQVRLTSLTACTFTLLVGAAPFDALSEPELIERQRLROELRARNYLNLSGGYQ 60
QY 61 ELERVVLRKPKHAGVQVRFAGSFYFAITVITIGYHAAAPSTDGKVFQCFMYALLGPI 120
Db 61 QELVILQSEPHRAGVQVRFAGSFYFAITVITIGYHAAAPSTDGKVFQCFMYAVLGIPL 120
QY 121 TLVVFQSLGERINTLVRLHRAKGLGMRRADVSNANVLLTGFPSCTSLCIGAAAFSH 180
Db 121 TLVVFQSLGERNTFVRLHRAKGLKCCCGNTEVSNVNTVGFPSGCG-LVPWAAAFSQ 179
QY 181 YEHWTFFQAYCYFTLITLTIIGFDVVALQKQALQTPQYVAFSVYILTLGLTVIGAFIN 240
Db 180 CEDWSFFHAYCYFTLITLTIIGFDVVALQKQALQKPPYVAFSVYILVGLTVIGAFIN 239
QY 241 LVVLRFTMTNAEDKRAEHRALLTNRN 267
Db 240 LVVLRFTMTNDEDLLEGEVAQILAGN 266

RESULT 12
CIW9_RAT
AC Q9ES08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
RA Coetzee W.A., Rudy B.;
RT "Kt3.2 and kt3.3, two novel human two-pore k(+) channels closely
RT related to TASK-1.";
RL J. Neurophysiol. 86:130-142(2001).
RN [2]
RP TISSUE SPECIFICITY.
RC MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045;
RA Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C.,
RA Grzeschik K.-H., Daut J., Karschin A.;
RT "Expression pattern in brain of TASK-1, TASK-3, and a tandem pore
RT domain K(+) channel subunit, TASK-5, associated with the central
RT auditory nervous system.";
RL Mol. Cell. Neurosci. 18:632-648(2001).
CC -! FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -! TISSUE SPECIFICITY: Expressed in the CNS but not in heart, lung,
CC liver, kidney, intestine and skeletal muscle. The highest
CC expression was found in the olfactory nuclei, piriform cortex,
CC cerebellum, antedorsal thalamic nucleus, pontine nucleus, dorsal
CC raphe and several nuclei in the medulla. Shows a non-homogeneous
CC distribution in the hippocampus. Expressed at highest levels in
CC the lateral posterior and inferior portions and at medium levels
CC in neocortex.
CC -! SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF257082; AAG33128.1; -.
CC RGD; 621451; Kcnk9.
CC InterPro; IPR003280; K+channel_2pore.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR005407; TASK3_channel.
CC InterPro; IPR003092; TASK3_channel.
CC PRINTS; PR01333; 2POREKCHANEL.
CC PRINTS; PR01585; TASK3CHANNEL.
CC PRINTS; PR01095; TASKCHANNEL.
CC Glycoprotein; Ion transport; Ionic channel; Potassium;
CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
FT DOMAIN 1 8
FT TRANSMEM 9 29
FT DOMAIN 78 101
FT DOMAIN 108 128
FT DOMAIN 129 158
FT TRANSMEM 159 179
FT DOMAIN 184 207
FT TRANSMEM 219 >237
FT CARBOHYD 53 53
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26674 MW; A44D2D32BE08A7DB CRC64;

Query Match 45.2%; Score 924; DB 1; Length 237;
Best Local Similarity 73.4%; Pred. No. 3.3e-65;
```

Matches 174; Conservative 26; Mismatches 37; Indels 0; Gaps 0;

QY 1 MKRQNVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSGGYE 60  
 DB 1 MKRQNVRLTSLIACITFTYLLVGAAVFDALSDHEMEEEKLKAEEVRLRGKYNISDDYQ 60

QY 61 ELERVVLRLKPKHAGVQWRPAGSFYFAITVITTTIGYCHAAAPSDGKVKFCMFYALLGIPL 120  
 DB 61 QLEVLTLQSEPHRAGVQWRPAGSFYFAITVITTTIGYCHAAAPSDGKVKFCMFYALLGIPL 120

QY 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSH 180  
 DB 121 TLVWFQSLGERMTFVRYLLKRIKCCGMRNTEVSMENWTVGFFSCMTLCIGAAAFSQ 180

QY 181 YEHWTFFQAYYYCFITLTITGFGDYVALQKDALQTPQYVAFSFYVILTGLTVIGA 237  
 DB 181 CEDWSFFHAYYYCFITLTITGFGDYVALQKDALQTPQYVAFSFYVILTGLTVIGA 237

RESULT 13  
 C1WF RAT STANDARD; PRT; 318 AA.  
 ID C1WF RAT 44.9%; Score 916.5; DB 1; Length 318;  
 AC Q8R5T0; Q920G1; Best Local Similarity 68.8%; Pred. No. 1.8e-64;  
 DT 28-FEB-2003 (Rel. 41, Created) Matches 185; Conservative 29; Mismatches 52; Indels 3; Gaps 3;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Potassium channel subfamily K member 15 (Acid-sensitive potassium  
 DE channel protein TASK-5) (TWIK-related acid-sensitive K+ channel 5)  
 DE (rTASK-5).  
 GN Names=Kcnk15; Synonyms=Task5;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. STRAIN=Long Evans; TISSUE=Brain;  
 RC Kawano T., Nakajima S., Nakajima Y.;  
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 82-318 FROM N.A.  
 RC STRAIN=Wistar;  
 RX MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045;  
 RA Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C.,  
 RA Grzeschik K.-H., Daut J., Karschin A.;  
 RT "Expression pattern in brain of TASK-1, TASK-3, and a tandem pore  
 RT domain K(+) channel subunit, TASK-5, associated with the central  
 RT auditory nervous system.";  
 RL Mol. Cell. Neurosci. 18:632-648 (2001).  
 CC -!- FUNCTION: Probable potassium channel subunit. No channel activity  
 CC observed in heterologous systems. May need to associate with  
 CC another protein to form a functional channel.  
 CC -!- SUBUNIT: Heterodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Brain-specific. Highly expressed in auditory  
 CC nuclei, in Purkinje cells and in olfactory bulb mitral cells.  
 CC -!- PTM: Phosphorylated (Potential).  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF467250; AAL77036.1; -;  
 CC EMBL; AF294353; AAK97094.1; -;  
 CC RGD; 619733; Kcnk15.  
 CC InterPro; IPR005821; Ion trans.  
 CC InterPro; IPR003280; K+channel\_2pore.

DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR008073; TASK5\_Channel.  
 DR InterPro; IPR003092; TASK\_Channel.  
 DR Pfam; PF00520; Ion trans. 1.  
 DR PRINTS; PR01333; 2POREKCHANEL.  
 DR PRINTS; PR01690; TASK5CHANNEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 KW Ion transport; Ionic channel; Potassium; Potassium channel;  
 KW Transmembrane; Transport; Voltage-gated channel.  
 FT DOMAIN 1 8 Cytoplasmic (Potential).  
 FT TRANSMEM 9 29 Potential.  
 FT DOMAIN 80 101 Pore-forming 1 (Potential).  
 FT TRANSMEM 108 128 Potential.  
 FT DOMAIN 129 158 Cytoplasmic (Potential).  
 FT TRANSMEM 159 179 Potential.  
 FT DOMAIN 189 209 Pore-forming 2 (Potential).  
 FT TRANSMEM 223 243 Potential.  
 FT DOMAIN 244 318 Cytoplasmic (Potential).  
 FT CONFLICT 315 315 R -> W (in Ref. 2).  
 SQ SEQUENCE 318 AA; 35651 MW; A06299212F56834ED CRC64;

Query Match 44.9%; Score 916.5; DB 1; Length 318;  
 Best Local Similarity 68.8%; Pred. No. 1.8e-64;  
 Matches 185; Conservative 29; Mismatches 52; Indels 3; Gaps 3;

QY 1 MKRQNVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSGGY 59  
 DB 1 MKRQNVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSGGY 59

QY 60 ELERVVLRLKPKHAGVQWRPAGSFYFAITVITTTIGYCHAAAPSDGKVKFCMFYALLGIPL 119  
 DB 60 ELERVVLRLKPKHAGVQWRPAGSFYFAITVITTTIGYCHAAAPSDGKVKFCMFYALLGIPL 119

QY 120 LTLVWFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFS 179  
 DB 120 LTLVWFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFS 179

QY 180 YEHWTFFQAYYYCFITLTITGFGDYVALQKDALQTPQYVAFSFYVILTGLTVIGAFL 239  
 DB 180 YEHWTFFQAYYYCFITLTITGFGDYVALQKDALQTPQYVAFSFYVILTGLTVIGAFL 239

QY 240 NLVLRFTWMADEKRDHRAHLLTRNG 268  
 DB 240 NLVLRFTWMADEKRDHRAHLLTRNG 268

RESULT 14  
 C1WF HUMAN STANDARD; PRT; 330 AA.  
 ID C1WF HUMAN 44.9%; Score 916.5; DB 1; Length 330;  
 AC Q9H427; Q9HBC8; Best Local Similarity 68.8%; Pred. No. 1.8e-64;  
 DT 28-FEB-2003 (Rel. 41, Created) Matches 185; Conservative 29; Mismatches 52; Indels 3; Gaps 3;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium channel subfamily K member 15 (Acid-sensitive potassium  
 DE channel protein TASK-5) (TWIK-related acid-sensitive K+ channel 5)  
 DE (Two pore potassium channel KT3.3).  
 GN Name=KCNK15; Synonyms=TASK5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. VARIANTS GLU-95; THR-260; HIS-261 AND LEU-323, AND  
 RP MUTAGENESIS OF ARG-138; 141-LEU-CYS-145; TRP-151 AND CYS-153.  
 RC TISSUE=Brain, Colon, and Ovarian carcinoma;  
 RX MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045;  
 RA Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C.,  
 RA Grzeschik K.-H., Daut J., Karschin A.;  
 RT "Expression pattern in brain of TASK-1, TASK-3, and a tandem pore  
 RT domain K(+) channel subunit, TASK-5, associated with the central  
 RT auditory nervous system.";  
 RL Mol. Cell. Neurosci. 18:632-648 (2001).  
 CC -!- FUNCTION: Probable potassium channel subunit. No channel activity  
 CC observed in heterologous systems. May need to associate with  
 CC another protein to form a functional channel.  
 CC -!- SUBUNIT: Heterodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Brain-specific. Highly expressed in auditory  
 CC nuclei, in Purkinje cells and in olfactory bulb mitral cells.  
 CC -!- PTM: Phosphorylated (Potential).  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF467250; AAL77036.1; -;  
 CC EMBL; AF294353; AAK97094.1; -;  
 CC RGD; 619733; Kcnk15.  
 CC InterPro; IPR005821; Ion trans.  
 CC InterPro; IPR003280; K+channel\_2pore.

RP SEQUENCE FROM N.A.  
RC TISSUE-Brain;  
RX MEDLINE=21324619; PubMed=11431495;  
RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,  
RA Coetzee W.A., Rudy B.;  
RT KT3.2 and KT3.3, two novel human two-pore K(+) channels closely  
RT related to TASK-1.;  
RL J. Neurophysiol. 86:130-142(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Ashmole I., Goodwin P.A., Stanfield P.R.;  
RT "TASK-5, a novel member of the tandem pore K+ channel family.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS GLU-95; THR-260 AND LEU-323.  
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggett C.L.,  
RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaeialtho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
CC -!- FUNCTION: Probable potassium channel subunit. No channel activity  
CC observed in heterologous systems. May need to associate with  
CC another protein to form a functional channel.  
CC -!- SUBUNIT: Heterodimer (Potential).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Detected in pancreas, heart, placenta, lung,  
CC liver, kidney, ovary and testis, and at lower levels in prostate  
CC and spleen.  
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
CC (TC 1.A.1.8) family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF294350; AAK97091.1; -;  
CC EMBL; AF294351; AAK97092.1; -;  
CC EMBL; AF294352; AAK97093.1; -;  
CC EMBL; AF257081; AAK93127.1; -;  
CC EMBL; AF336342; AAK37518.1; -;  
CC EMBL; AL118522; CAC14068.1; -;  
CC GenBank; HGNC:13614; KCKN35.  
CC MIM; 607368; -;  
CC InterPro; IPR003280; K+channel\_2pore.  
CC InterPro; IPR001622; K+channel\_pore.  
CC InterPro; IPR008073; TASK5\_channel.

DR InterPro; IPR003092; TASK\_channel.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01890; TASK5CHANNEL.  
KW Ion transport; Ionic channel; Polymorphism; Potassium;  
KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
FT DOMAIN 1 8.  
FT TRANSMEM 9 29  
FT DOMAIN 80 101  
FT TRANSMEM 108 128  
FT DOMAIN 129 158  
FT TRANSMEM 159 179  
FT DOMAIN 189 209  
FT TRANSMEM 223 243  
FT DOMAIN 244 330  
FT VARIANT 95 95  
FT VARIANT 260 260  
FT VARIANT 261 261  
FT VARIANT 323 323  
FT VARIANT 138 138  
FT MUTAGEN 141 145  
FT MUTAGEN 151 151  
FT MUTAGEN 153 153  
FT SEQUENCE 330 AA; 36130 MW; AA2A54D0615BC53C CRC64;  
Query Match 41.4%; Score 846; DB 1; Length 330;  
Best Local Similarity 64.7%; Pred. No. 7.4e-59;  
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;  
QY 1 MKRONVRLALIVCTFTLVGAADFALSEPELIEROLRQELRARNYLSGGYE 60  
DB 1 MRRSVRAAGLVCTCLVLLVGAADFALSESGRQLLVQKRGALRRKFGFAEDYR 60  
QY 61 ELERVLLRLKPKAGVQWRFGAGSFYAITVTITTYGHAAPSTDGKVFVCMFYALLGLPL 120  
DB 61 ELERLALQAEPRAGRWKFGSGFYAITVTITTYGHAAPSTDGKVFVCMFYALLGLPL 120  
QY 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRRADYVSMANWLVIGFPFSCISTLCIGAAAFSH 180  
DB 121 TLVTFQSLGERLNNAVRELLAAKCLGLRWTCVSTENLVAGLLACAAATLALGAVAFSH 180  
QY 181 YEHWTFFQAYYCFITLTITIGFDYVALQKQDQALQTPQYVAFSFWITLTGLTVIGAFIN 240  
DB 181 FEGWTFHAYYCFITLTITIGFDYVALQKQDQALQKLPYVAFSFLYLLGLTVIGAFIN 240  
QY 241 LVVLRFTMTNADEKRD 258  
DB 241 LVVLRFLVASADWPERRA 258  
ID O17185 PRELIMINARY; PRT; 329 AA.  
AC O17185; O76795;  
DT 01-JAN-1998 (TRENDELrel. 05, Created)  
DT 01-OCT-2001 (TRENDELrel. 18, Last sequence update)  
DE 25-OCT-2004 (TRENDELrel. 28, Last annotation update)  
DE Suppressor protein 9 (Putative potassium channel subunit n2p38) (Two-  
DE pore K+ channel).  
GN Name-sup-9; ORFNames=F34D6.3;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
RX NCBI\_TaxID=6239;  
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Murray J., Wohldmann P., O'Neal D.;
RT "The sequence of C. elegans cosmid F34D6. ";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salkoff L.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=22896676; PubMed=14534247;
RA de la Cruz I.P., Levin J.Z., Cummins C., Anderson P., Horvitz H.R.;
RT "sup-9, sup-10, and unc-93 may encode components of a two-pore K+
RT channel that coordinates muscle contraction in Caenorhabditis
RT elegans. ";
RL J. Neurosci. 23:9133-9145(2003).
RN [8]
RP SEQUENCE FROM N.A.
RA Perez de la Cruz I., Horvitz H.R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
DR EMBL; AF025454; AAC71151.2; -
DR EMBL; AF083652; AAC32863.1; -
DR EMBL; AY357729; AAC84518.1; -
DR PIR; T32347; T32347.
DR PIR; T43509; T43509.
DR WormBase; WBGene0006318; sup-9.
DR WormPep; F34D6.3; CE28297.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FOREKCHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;

```

Query Match 40.2%; Score 820; DB 2; Length 329;

Best Local Similarity 48.3%; Pred. No. 8 5e-57;

Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;

QY 1 MKRQNVRLALIVCTTLLVGAADFALAESEPELIERQRLRQQLRARNVLSQGYE 60

```

Db 1 MKRQNVRLALIVCTTLLVGAADFALAESEPELIERQRLRQQLRARNVLSQGYE 60
QY 61 ELERVVLRRLKPKAGVQWRFAGSFYPAITVITTTIGYCHAAPSTDGKGVFCMFYALIGIPL 120
Db 61 ILEATIVKSVPHKAGVQWKFSGAFYFATVITTTIGYGHSTPMTDAGKGVFCMLYALAGIPL 120
QY 121 TLVMPQSLGERINTLVRYLLHRAKGLGMRRADVSMANMVLIGFFSCISTLCI--GAAAF 178
Db 121 GLIMFQSIGERMNTFAAKLLRFRRAAG-KQPIVTSDDLII--FCTGWGGLLIFGGAFMF 177
QY 179 SHVEHWTFQAYYYCYFILTITTTIGFDYVALQDQALQTOPOYVAFSVVYILTGLTWTIGAF 238
Db 178 SSTENWTFDAVYCFVLTITTTIGFDYVALQKRGSLQTOPEYVFFSLVFLFGLTWTISAA 237
QY 239 LNLVLVLRFMNTMAEDEKRDAAEHRAL----LTRNGQAGGGGGGSAHTTTDTASTAAAGGG 294
Db 238 MNLVLVLRFLTMNTEDERRDEQEAIIAAQGLVVRVGDPTADDGRLPLSDNVSLAS----- 292
QY 295 GFRNVYAEVLHFQSMCSCMLWYKSRKLYQSIPIPIPRDLSTSDTCVEQSHSSPGGG 350
Db 293 -----CSC-YQLPDEKLRHR-----HRKHTEPHGG 316

```

Search completed: July 13, 2005, 08:44:33

Job time : 92.0757 secs



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:58:54 ; Search time 97.2039 Seconds  
(without alignments)  
1567.669 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MKRQVRILALIVCTFYLL.....STGLSLSTFRLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	AAE10343	Aae10343 Murine TA
2	2042	100.0	394	AAY79674	Aay79674 Human pot
3	2042	100.0	394	AAY87291	Aay87291 Human sig
4	2042	100.0	394	ADI27924	Adi27924 Human pro
5	2042	100.0	394	ADI27925	Adi27925 Human pro
6	2042	100.0	395	ADI27915	Adi27915 Human pro
7	1850.5	90.6	412	ADI27916	Adi27916 Rat prote
8	1819	89.1	405	AAV95230	Aay95230 Mouse pot
9	1235.5	60.5	309	AAU07620	Aau07620 Mouse 2P
10	1116	54.7	374	AAI18807	Aai18807 Amino aci
11	1116	54.7	374	AAI18813	Aai18813 Protein e
12	1116	54.7	374	AAE33938	Aag33938 Amino aci
13	1116	54.7	374	AAE13279	Aae13279 Human tra
14	1116	54.7	374	AAE22989	Aae22989 Human TWI
15	1116	54.7	374	ADI27948	Adi27948 Human TWI
16	1116	54.7	376	ADR66129	Adr66129 Human pro
17	1116	54.7	376	ADR66471	Adr66471 Human pro
18	846	41.4	330	ADB80478	Adb80478 Ovarian c
19	846	41.4	400	AAE10679	Aae10679 Human TWI
20	846	41.4	400	ADI27912	Adi27912 Human TWI
21	838	41.0	330	AAAB4734	Aab47334 FCTR11. 8
22	838	41.0	330	ADK18422	Adk18422 Human NOV
23	838	41.0	400	AAE10678	Aae10678 Human TWI
24	838	41.0	400	AAE13286	Aae13286 Human tra
25	838	41.0	400	ADI27909	Adi27909 Human TWI

26	785.5	38.5	436	4	ABG29273	Abg29273 Novel hum
27	777	38.1	340	4	ABB64375	Abb64375 Drosophil
28	774	37.9	279	4	AAM14676	Aam14676 Peptide #
29	774	37.9	279	4	ABB33636	Abb33636 Peptide #
30	774	37.9	279	4	AAM27095	Aam27095 Peptide #
31	774	37.9	279	4	ABB28454	Abb28454 Peptide #
32	774	37.9	279	4	ABB19091	Abb19091 Protein #
33	774	37.9	279	4	AAM66810	Aam66810 Human bon
34	774	37.9	279	4	AAM54409	Aam54409 Human bra
35	774	37.9	279	4	ABG48478	Abg48478 Human liv
36	774	37.9	279	4	AAM02399	Aam02399 Peptide #
37	774	37.9	279	5	ABG36465	Abg36465 Human pep
38	773	37.9	408	4	AA31804	Aab31804 Amino aci
39	742	36.3	398	4	ABE71787	Abb71787 Drosophil
40	619	30.3	212	6	ABO14995	ABO14995 Human NOV
41	379	18.6	361	4	AA31805	Aab31805 Amino aci
42	373	18.3	491	8	ABO84626	ABO84626 Mouse can
43	370	18.1	411	3	AAE10342	Aae10342 Murine TR
44	369	18.1	370	2	AAV30648	Aay30648 A mechani
45	369	18.1	411	2	AAV28497	Aay28497 Mouse h-T

## ALIGNMENTS

## RESULT 1

AAE10343  
ID AAE10343 standard; protein; 394 AA.

AC AAE10343;

XX  
DT 10-DEC-2001 (first entry)

XX  
DE Murine TASK potassium channel protein.

XX  
KW Murine; potassium channel protein; TREK-1; TASK; anaesthetic; analgesia;

XX  
OS Mus sp.

XX  
PN WO200047738-A2.

XX  
PD 17-AUG-2000.

XX  
PF 11-FEB-2000; 2000WO-IB0000226.

XX  
PR 12-FEB-1999; 99US-0119727P.

XX  
PR 11-FEB-2000; 2000US-00503089.

XX  
(CNRS ) CNRS CENT NAT RECH SCI.

XX  
Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;

XX  
WPI; 2000-549146/50.

PT Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic properties.

PS Claim 23; Page 34-35; 39pp; English.

XX The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TASK potassium channel protein related to the invention

SQ Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 3; Length 394;

Best Local Similarity 100.0%; Pred. No. 5.3e-213; Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRLARYNLSQGGYE 60	
Db 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRLARYNLSQGGYE 60	
QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYGHAAAPSTDGKVFYALLGIPL 120	
Db 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYGHAAAPSTDGKVFYALLGIPL 120	
QY 121 TLVMPQSIGERINTLVRYLLHRAKGLGMRADVSMMANVLIIGFSCISTLICIGAAAFSH 180	
Db 121 TLVMPQSIGERINTLVRYLLHRAKGLGMRADVSMMANVLIIGFSCISTLICIGAAAFSH 180	
QY 181 YEHWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSVYILTLGLTVIGAFIN 240	
Db 181 YEHWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSVYILTLGLTVIGAFIN 240	
QY 241 LVVLFMTMNAEDEKRDHRAHLLTRNGQAGGGGGGSAHTTDTASSTAAAGGGFRNVY 300	
Db 241 LVVLFMTMNAEDEKRDHRAHLLTRNGQAGGGGGGSAHTTDTASSTAAAGGGFRNVY 300	
QY 301 AEVLHFQSMCSCLWYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360	
Db 301 AEVLHFQSMCSCLWYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360	
QY 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394	
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394	
RESULT 2	
AAAY79674	
ID	AAAY79674 standard; protein; 394 AA.
AC	AAAY79674;
XX	
DT	29-AUG-2000 (first entry)
DE	Human potassium channel TASK1.
XX	
KW	TASK1; TWIK-related acid-sensitive K+ channel 1; human;
KW	potassium channel; drug screening; hypertension; hypotensive; epilepsy;
KW	arrhythmia; vascular diseases; neurodegenerative disease; ischaemia;
KW	anoxia; endocrine disease; muscle disease; therapy.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 53 /note= "N-glycosylated"
FT	Modified-site 323 /note= "O-phosphorylated"
FT	Modified-site 383 /note= "O-phosphorylated"
FT	Modified-site 392 /note= "O-phosphorylated"
FT	Modified-site 393 /note= "O-phosphorylated"
FT	Modified-site /note= "O-phosphorylated"
XX	
PN	WO200027871-A2.
XX	
PD	18-MAY-2000.
XX	
PF	09-NOV-1999; 99WO-IB001886.
XX	
PR	09-NOV-1998; 98US-0107692P.
PR	08-NOV-1999; 99US-00436265.
XX	
PA	(CNRS ) CNRS CENT NAT RECH SCI.
XX	
PI	Duprat F, Lesage F, Lazdunski M;

XX	WPI: 2000-376487/32.
DR	N-PSDB; AAA27746.
XX	
PT	New nucleic acid encoding a non-inactivating outwardly rectifying
PT	potassium transport channel, designated TASK2, useful in the treatment of
PT	hypertension or dysfunctions of the kidney, liver or pancreas.
XX	
PS	Disclosure; Fig 8; 9lpp; English.
XX	
CC	The present sequence is that of human TASK1 (TWIK-related acid-sensitive
CC	K+ channel), a member of a new family of 2P domain potassium channels,
CC	also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675).
CC	TASK1 is expressed in many different tissues, and at particularly high
CC	levels in pancreas and placenta. Host cells expressing TWIK-1 family
CC	members can be used to screen for substances that modulate the activity
CC	of members of the TWIK-1 family of potassium channels. The drugs
CC	identified may be useful in the treatment of diseases of the heart or of
CC	the nervous system, such as epilepsy, arrhythmia, vascular diseases,
CC	neurodegenerative diseases, kidney, liver or pancreas diseases,
CC	hypertension, diseases associated with ischaemia or anoxia, endocrine
CC	diseases associated with anomalies of hormone secretion, and muscle
CC	diseases
SQ	Sequence 394 AA;
Query Match 100.0%; Score 2042; DB 3; Length 394;	
Best Local Similarity 100.0%; Pred. No. 5.3e-213; Mismatches 0; Indels 0; Gaps 0;	
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRLARYNLSQGGYE 60	
Db 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRLARYNLSQGGYE 60	
QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYGHAAAPSTDGKVFYALLGIPL 120	
Db 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYGHAAAPSTDGKVFYALLGIPL 120	
QY 121 TLVMPQSIGERINTLVRYLLHRAKGLGMRADVSMMANVLIIGFSCISTLICIGAAAFSH 180	
Db 121 TLVMPQSIGERINTLVRYLLHRAKGLGMRADVSMMANVLIIGFSCISTLICIGAAAFSH 180	
QY 181 YEHWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSVYILTLGLTVIGAFIN 240	
Db 181 YEHWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSVYILTLGLTVIGAFIN 240	
QY 241 LVVLFMTMNAEDEKRDHRAHLLTRNGQAGGGGGGSAHTTDTASSTAAAGGGFRNVY 300	
Db 241 LVVLFMTMNAEDEKRDHRAHLLTRNGQAGGGGGGSAHTTDTASSTAAAGGGFRNVY 300	
QY 301 AEVLHFQSMCSCLWYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360	
Db 301 AEVLHFQSMCSCLWYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360	
QY 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394	
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394	
RESULT 3	
AAAY87291	
ID	AAAY87291 standard; protein; 394 AA.
AC	AAAY87291;
XX	
DT	11-MAY-2000 (first entry)
XX	
XX	Human signal peptide containing protein HSpp-68 SEQ ID NO:68.
DE	Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
XX	inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW	antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW	antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
XX muscular dystrophy.  
OS Homo sapiens.  
XX WO200000610-A2.  
XX 06-JAN-2000.  
XX 25-JUN-1999; 99WO-US014484.  
XX 26-JUN-1998; 98US-0090762P.  
XX 31-JUL-1998; 98US-0094983P.  
XX 01-OCT-1998; 98US-0102686P.  
XX 11-DEC-1998; 98US-0112129P.  
XX (INCY-) INCYTE PHARM INC.  
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX WPI; 2000-160673/14.  
XX N-PSDB; AA298176.  
XX New human signal peptide-containing proteins useful in treatment.  
XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
XX disease.  
XX Claim 1; Page 207-208; 327pp; English.  
XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the  
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
XX neuroprotective, cardiovascular and antiasthmatic activities, and can be  
XX used in gene therapy. HSPs can be used to treat or prevent disorders  
XX associated with decreased activity or function of HSP. Antagonists of  
XX HSP are used to treat or prevent disorders associated with increased  
XX activity or function of HSP. Such diseases include cell proliferation  
XX (including cancer), inflammation, cardiovascular, neurological,  
XX reproductive or developmental disorders, (e.g. arteriosclerosis,  
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
XX asthma, Crohn's disease, microbial or other infections, congestive or  
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
XX nucleic acids can be used for the recombinant production of HSP, for  
XX detecting HSP in standard hybridisation and amplification assays (for  
XX diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
XX or ribozyme therapeutics, for detecting related sequences or genetic  
XX variations, and for chromosomal mapping. HSP are also used to raise  
XX specific antibodies (Ab) and to screen for agonists and antagonists  
XX (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP  
XX -related diseases (in usual immunoassays), as therapeutic antagonists, in  
XX competitive drug screens, and for purification of HSP from natural  
XX sources  
XX SQ Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 5.3e-213;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQVRLALIVCTTLLVGAADFALDESEPELIERQRLERQQLERARVNLSCGGYE 60  
DB 1 MKRQVRLALIVCTTLLVGAADFALDESEPELIERQRLERQQLERARVNLSCGGYE 60  
QY 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDDGKVFQCMFVALLIGIPL 120  
DB 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDDGKVFQCMFVALLIGIPL 120

QY 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSH 180  
DB 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSH 180  
QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAEIN 240  
DB 181 YEHWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAEIN 240  
QY 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGPRNVY 300  
DB 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGPRNVY 300  
QY 301 AEVLHFQSMCSCLVYKRSREKQYSIPMIIPRLDLSDTCEQSHSPGCGGRYSDTPSRR 360  
DB 301 AEVLHFQSMCSCLVYKRSREKQYSIPMIIPRLDLSDTCEQSHSPGCGGRYSDTPSRR 360  
QY 361 CLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394  
DB 361 CLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394

RESULT 4  
ADI27924  
ID ADI27924 standard; protein; 394 AA.  
XX  
AC ADI27924;  
XX  
XX 06-MAY-2004 (first entry)  
DT Human protein #2.  
DE  
XX  
XX Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;  
KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;  
KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;  
KW antiparkinsonian; hepatotropic; cardiovascular.  
XX Homo sapiens.  
XX US2003165891-A1.  
XX 04-SEP-2003.  
XX 15-MAY-2002; 2002US-00146733.  
XX 29-FEB-2000; 2000US-00515520.  
XX 29-FEB-2000; 2000US-0185938P.  
XX 03-MAR-2000; 2000US-00518886.  
XX 07-APR-2000; 2000US-0195734P.  
XX 11-APR-2000; 2000US-0195993P.  
XX 26-APR-2000; 2000US-0199799P.  
XX 19-SEP-2000; 2000US-0233537P.  
XX 25-SEP-2000; 2000US-0235018P.  
XX 25-SEP-2000; 2000US-0235059P.  
XX 15-DEC-2000; 2000US-0256240P.  
XX 18-DEC-2000; 2000US-0256588P.  
XX 21-DEC-2000; 2000US-0258028P.  
XX 28-FEB-2001; 2001US-00796720.  
XX 06-APR-2001; 2001US-00828035.  
XX 11-APR-2001; 2001US-00833081.  
XX 25-APR-2001; 2001US-00843128.  
XX 19-SEP-2001; 2001US-00957683.  
XX 25-SEP-2001; 2001US-00964252.  
XX 25-SEP-2001; 2001US-00964256.  
XX 17-DEC-2001; 2001US-00024623.  
XX (MILL-) MILLENNIUM PHARM INC.  
PA Curtis RAJ, Glucksmann MA, Silos-Santiago I;  
PI WPI; 2004-069000/07.  
XX TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,  
PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for

PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and  
PT cardiovascular disorders.

XX Disclosure; SEQ ID NO 17; 638pp; English.

XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,  
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel  
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,  
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and  
CC 53763 ICF nucleic acids and proteins may be used for preventing,  
CC diagnosing and treating ICF-related diseases. The sequences may be used  
CC to treat disorders associated with decreased expression by rectifying  
CC mutations or deletions in a patient's genome that affect the activity of  
CC ICF proteins by expressing inactive proteins or to supplement the  
CC patients own production of ICF proteins. The proteins may also be used as  
CC antigens in the production of antibodies against ICF proteins and in  
CC assays to identify modulators of ICF protein expression and activity. The  
CC anti-ICF protein antibodies, agonists and antagonists may be used to  
CC regulate ICF protein expression and activity. The antibodies may also be  
CC used as diagnostic agents for detecting the presence of ICF proteins in  
CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used  
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers  
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple  
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This  
CC sequence represents a human protein used in the scope of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 8; Length 394;  
Best Local Similarity 100.0%; Pred. No. 5.3e-213;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQOELRARNYLSQGGYE 60  
DB 1 MKRQVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQOELRARNYLSQGGYE 60  
QY 61 ELERVVLRLKPKHAGVQWRFGAGFYFAITVITTCYGHAAPESTDGKVCFCFYALLGIPL 120  
DB 61 ELERVVLRLKPKHAGVQWRFGAGFYFAITVITTCYGHAAPESTDGKVCFCFYALLGIPL 120  
QY 121 TLVVFQSLGERINTLVRYLLHRAKGLMRRADVSMANNVLIIGFFSCISTLCIGAAAFSH 180  
DB 121 TLVVFQSLGERINTLVRYLLHRAKGLMRRADVSMANNVLIIGFFSCISTLCIGAAAFSH 180  
QY 181 YEHWTFFQAYYCYFTLTTIGFGDVVALQKQALOTQPYVAFSVYILTGLTVIGAFIN 240  
DB 181 YEHWTFFQAYYCYFTLTTIGFGDVVALQKQALOTQPYVAFSVYILTGLTVIGAFIN 240  
QY 241 LVVLRPMTWNADEKRDRAHRLALTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300  
DB 241 LVVLRPMTWNADEKRDRAHRLALTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300  
QY 301 AEVLHFQSMCSLWYKREKLYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360  
DB 301 AEVLHFQSMCSLWYKREKLYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360  
QY 361 CLCSGAPRAISVSSTGLHSLSTFRLMKRRSSV 394  
DB 361 CLCSGAPRAISVSSTGLHSLSTFRLMKRRSSV 394

RESULT 5

AD127925

ID AD127925 standard; protein; 394 AA.

XX

AC AD127925;

XX

DT 06-MAY-2004 (first entry)

XX Human protein #3.

DE

XX

KW

KW

KW

KW

XX

OS

XX

PN

XX

XX

PD

XX

PP

XX

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;  
Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;  
cardiovascular disorder; cytostatic; neuroprotective; nootropic;  
antiparkinsonian; hepatotropic; cardiovascular.

Homo sapiens.

US2003165891-A1.

04-SEP-2003.

15-MAY-2002; 2002US-00146733.

29-FEB-2000; 2000US-00515520.

29-FEB-2000; 2000US-0185938P.

03-MAR-2000; 2000US-00518866.

07-APR-2000; 2000US-0195734P.

11-APR-2000; 2000US-0195993P.

26-APR-2000; 2000US-0199799P.

19-SEP-2000; 2000US-0233537P.

25-SEP-2000; 2000US-0235018P.

15-DEC-2000; 2000US-0256240P.

18-DEC-2000; 2000US-0256588P.

21-DEC-2000; 2000US-0258028P.

28-FEB-2001; 2001US-00796720.

06-APR-2001; 2001US-00828035.

11-APR-2001; 2001US-00833081.

25-APR-2001; 2001US-00843328.

19-SEP-2001; 2001US-00957683.

25-SEP-2001; 2001US-00964252.

25-SEP-2001; 2001US-00964256.

17-DEC-2001; 2001US-00024623.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ, Glucksmann MA, Silos-Santiago I;

WPI; 2004-069000/07.

TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,  
alphadelta-4, 54414, or 53763 nucleic acids and proteins, useful for  
preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and  
cardiovascular disorders.

Disclosure; SEQ ID NO 18; 638pp; English.

The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,  
IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel  
family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,  
TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and  
53763 ICF nucleic acids and proteins may be used for preventing,  
diagnosing and treating ICF-related diseases. The sequences may be used  
to treat disorders associated with decreased expression by rectifying  
mutations or deletions in a patient's genome that affect the activity of  
ICF proteins by expressing inactive proteins or to supplement the  
patients own production of ICF proteins. The proteins may also be used as  
antigens in the production of antibodies against ICF proteins and in  
assays to identify modulators of ICF protein expression and activity. The  
anti-ICF protein antibodies, agonists and antagonists may be used to  
regulate ICF protein expression and activity. The antibodies may also be  
used as diagnostic agents for detecting the presence of ICF proteins in  
samples (e.g. by immunoassay). The nucleic acids and proteins may be used  
to prevent, diagnose and treat a wide variety of disorders, e.g. cancers  
and leukaemia, Alzheimer's disease, Parkinson's disease, multiple  
sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This  
sequence represents a human protein used in the scope of the invention.  
Note: The sequence data for this patent is also available in electronic  
format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 8; Length 394;

PR	25-SEP-2001; 2001US-00964256.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</
----	-------------------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

RESULT 7  
ADI27916  
ID ADI27916 standard; protein; 412 AA.  
XX  
AC ADI27916;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Rat protein #1.  
DE  
XX Rat; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;  
KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;  
KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;  
KW antiparkinsonian; hepatotropic; cardiovascular.  
XX  
OS Rattus norvegicus.  
XX  
XX US2003165891-A1.  
XX  
XX PD 04-SEP-2003.  
XX  
XX PF 15-MAY-2002; 2002US-00146733.  
XX  
XX PR 29-FEB-2000; 2000US-00515520.  
XX PR 29-FEB-2000; 2000US-0185938P.  
XX PR 03-MAR-2000; 2000US-00518866.  
XX PR 07-APR-2000; 2000US-0195734P.  
XX PR 11-APR-2000; 2000US-0195993P.  
XX PR 26-APR-2000; 2000US-0199799P.  
XX PR 19-SEP-2000; 2000US-0233537P.  
XX PR 25-SEP-2000; 2000US-0235018P.  
XX PR 25-SEP-2000; 2000US-0235059P.  
XX PR 18-DEC-2000; 2000US-0256240P.  
XX PR 21-DEC-2000; 2000US-0256588P.  
XX PR 28-FEB-2001; 2000US-00796720.  
XX PR 06-APR-2001; 2001US-00828035.  
XX PR 11-APR-2001; 2001US-00833081.  
XX PR 25-APR-2001; 2001US-00843128.  
XX PR 19-SEP-2001; 2001US-00957683.  
XX PR 25-SEP-2001; 2001US-00964252.  
XX PR 25-SEP-2001; 2001US-00964256.  
XX PR 17-DEC-2001; 2001US-00024623.  
XX  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX PI Curtis RAJ, Glucksmann MA, Silos-Santiago I;  
XX  
XX DR WPI; 2004-069000/07.  
XX  
XX PT TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,  
PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for  
PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and  
PT cardiovascular disorders.  
XX  
XX PS Disclosure; SEQ ID NO 9; 638pp; English.  
XX  
XX CC The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,  
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel  
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,  
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and  
CC 53763 ICF nucleic acids and proteins may be used for preventing,  
CC diagnosing and treating ICF-related diseases. The sequences may be used  
CC to treat disorders associated with decreased expression by rectifying  
CC mutations or deletions in a patient's genome that affect the activity of  
CC ICF proteins by expressing inactive proteins or to supplement the  
CC patients own production of ICF proteins. The proteins may also be used as  
CC antigens in the production of antibodies against ICF proteins and in  
CC assays to identify modulators of ICF protein expression and activity. The  
CC anti-ICF protein antibodies, agonists and antagonists may be used to  
CC regulate ICF protein expression and activity. The antibodies may also be  
CC used as diagnostic agents for detecting the presence of ICF proteins in

CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used  
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers  
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple  
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This  
CC sequence represents a rat protein used in the scope of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX SQ Sequence 412 AA;

Query Match 90.6%; Score 1850.5; DB 8; Length 412;  
Best Local Similarity 88.3%; Pred. No. 4.1e-192;  
Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;  
Qy 1 MKRQVRLALIVCTFTYLLVGAADFALDSEPELIERQRLERQLELRARYNLSGGYE 60  
Db 2 MKRQVRLALIVCTFTYLLVGAADFALDSEPELIERQRLERQLELRARYNLSGGYE 61  
Qy 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAFPSTGGKVFYALLGIPL 120  
Db 62 ELERVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAFPSTGGKVFYALLGIPL 121  
Qy 121 TLVNFQSLGERINTLVYLLHRAKGLGMRPADVSMANVLI GFSCISTICIGNAAFSH 180  
Db 122 TLVNFQSLGERINTLVYLLHRAKGLGMRPADVSMANVLI GFVSCISTICIGNAAFSY 181  
Qy 181 YEHWTFFQAYYYCFTLTITIGFDVVALQDQALQTPQYVAFSFVYLTGLTVIGAFNL 240  
Db 182 YERWTFFQAYYYCFTLTITIGFDVVALQDQALQTPQYVAFSFVYLTGLTVIGAFNL 241  
Qy 241 LVVLRFTMNAEDEKRAEHRALLTRNGAQGGGGG-----GGSANHTTTASSTAAA- 291  
Db 242 LVVLRFTMNAEDEKRAEHRALLTRNGAQGGGSLGSLGSDGVRPDPVTCAAAAG 301  
Qy 292 -----GGGGRNVVAVLVHFSQSMCSCLWYKREKLOYIPMIIPDLSTSDTCVQS 343  
Db 302 GMGVGVGVGGGFRNVVAVMLHFSQSMCSCLWYKREKLOYIPMIIPDLSTSDTCVQS 361  
Qy 344 HSSPGGGGRYSDTPSRRLCSGAPRSATSSVSTGLHSLSTPRGLMKRRSSV 394  
Db 362 HSSPGGGGRYSDTPSHPCLSGTQRTSAISSVSTGLHSLATPRGLMKRRSSV 412

RESULT 8

AAV95230  
ID AAV95230 standard; protein; 405 AA.  
XX  
XX AC AAV95230;  
XX  
XX DT 29-AUG-2000 (first entry)  
XX  
XX DE Mouse potassium channel TASK.

XX KW TASK; TWIK-related acid-sensitive K+ channel; mouse; potassium channel;  
KW drug screening; hypertension; hypotensive; epilepsy; arrhythmia;  
KW vascular diseases; neurodegenerative disease; ischaemia; anoxia;  
KW endocrine disease; muscle disease; therapy.

XX OS Mus musculus.

XX Key Location/Qualifiers  
XX Modified-site 50  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 334  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 403  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 404  
FT Modified-site /note= "O-phosphorylated"

XX WO200027871-A2.

XX 18-MAY-2000.

PD





```

AC AAB18807;
XX
DT 22-JAN-2001 (first entry)
DE
DE Amino acid sequence of a human DKN1 polypeptide.
KW Human; DKN1; potassium channel; cancer; pulmonary disease; depression;
KW cardiovascular disease; inflammatory disease; renal disease; pain;
KW psychiatric disorder; schizophrenia; neurodegenerative disease;
KW Alzheimer's disease; neurological disorder; migraine; epilepsy;
KW sleep-related disorder; erectile dysfunction; alopecia.
XX
OS Homo sapiens.
XX
XX WO200053628-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-EP001750.
XX
XX 05-MAR-1999; 99GB-00005061.
XX
XX 10-FEB-2000; 2000GB-00003112.
XX
XX (SMIK ) SMITHLINE BEECHAM PLC.
XX
XX Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;
XX
XX WPI; 2000-587424/55.
XX
XX N-PSDB; AAA75886.
XX
XX Polypeptides and polynucleotides of the potassium channel family, useful
XX for identifying agonists/antagonists of therapeutic use and diagnosis and
XX treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
XX disease.
XX
XX Claim 1; Page 25; 36pp; English.
XX
XX The present sequence represents human DKN1 polypeptide. The polypeptide
XX is a member of the potassium channel family. The DKN1 polypeptides and
XX polynucleotides are useful for treating diseases including cancer,
XX pulmonary, cardiovascular, inflammatory or renal diseases, pain,
XX psychiatric disorders including depression and schizophrenia,
XX neurodegenerative disease including Alzheimer's, neurological disorders,
XX migraine, epilepsy, sleep-related disorders, erectile dysfunction and
XX alopecia. DKN1 polynucleotides are useful as diagnostic reagents for
XX detecting mutations in the associated gene
XX
XX Sequence 374 AA;
XX
XX Query Match 54.7%; Score 1116; DB 3; Length 374;
XX Best Local Similarity 59.0%; Pred. No. 3.5e-112;
XX Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;
XX
QY 1 MKRQNVRLALIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
DB 1 MKRQNVRLSLIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
QY 61 ELERVVLRLKPKHAGVQWRPAGSFYFAITVITIGYGHAAFPSTGGKVFCEMFLGIGPL 120
DB 61 QLELVILQSEPHRAGVQWRPAGSFYFAITVITIGYGHAAFPSTGGKVFCEMFLGIGPL 120
QY 121 TLVMPQSLGERINTLVYLLHRAKGLGMRADVSMANNVLIGFPSCISTLCIGAAAFSH 180
DB 121 TLVMPQSLGERNMTFVYLLHRAKGLGMRADVSMANNVLIGFPSCISTLCIGAAAFSH 180
QY 181 YEHWTFQAYYYCFITLTITIGFDYVALQDQALQTPQYAFSFYILTLGTVIGAFIN 240
DB 181 CEWSFFHAYYYCFITLTITIGFDYVALQDQALQTPQYAFSFYILTLGTVIGAFIN 240
QY 241 LVVLRPMTVADEKRAHRLALFTNGOAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300
DB 241 LVVLRFLTNSEDRDAERASL-----AGNRNSWVIHIPEPRPS-----RPRY 286

```

Db 61 QLELVILQSEPHRAGVQWKFAAGFYFAITVITTTIGYHAAFGTDAGKAFCMFYAVLGIPL 120  
Qy 121 TLVMFQSLGERINTLVYLLHRAKKGLGMRRADVSMANMVLIGFFSCITSLCIGAAAFSH 180  
Db 121 TLVMFQSLGERMNTFVYLLKRIKKCGMRNTDVS MENMVTGFFSCMGTLCIGAAAFSQ 180  
Qy 181 YEHWTFFQAYYYCIFTITTTIGFGDYVALQKDQALQTOPOVYVAFSVVYLLTGLTVIGAFNL 240  
Db 181 CEWSFFHAYYYCIFTITTTIGFGDYVALQKDQALQKPLVYVAFSFMVILVGLTVIGAFNL 240  
Qy 241 LVLRFMTWNAEDKRAEHRALTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNVY 300  
Db 241 LVLRFMTWNSDEDRDAERASL-----AGNRNSMVIHPEPRPS-----RPRY 286  
Qy 301 -AEVLHFQSMCCLWYKSRKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359  
Db 287 KADVPDLQSVCSCTCYRSQD---YGRSVAPQNSFSAKLAPHYFHSYKIEISPSSTLK 343  
Qy 360 RCLCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394  
Db 344 NSLFP-----SPISSISPLHSFTDHQRLMKRRKSV 374

## RESULT 12

AAG63938  
ID AAG63938 standard; protein; 374 AA.

AC AAG63938;

XX AAG63938;

XX AAG63938;

DT 29-OCT-2001 (first entry)

XX Amino acid sequence of human potassium channel protein KCNB.

XX Human; potassium channel protein; KCNB; breast tissue; cancer; stroke;

XX potassium channel-associated disorder; brain associated disorder;

XX epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis;

XX migraine; psychiatric disorder; depression; schizophrenia; diabetes;

XX bipolar disease; heart disease; arrhythmia; pancreas disease;

XX pancreatitis.

XX Homo sapiens.

XX WO200166741-A2.

XX 13-SEP-2001.

XX 02-MAR-2001; 2001WO-US006801.

XX 03-MAR-2000; 2000US-0186915P.

XX (TULA-) TULARIK INC.

XX Mu D, Powers S;

XX WPI; 2001-522949/57.

XX N-PSDB; AAH74999.

XX A nucleic acid encoding a potassium channel, termed KCNB (potassium

channel expressed in breast), useful in the diagnosis, prognosis or

treatment of diseases associated with altered KCNB activity or

expression, e.g. cancer and diabetes.

XX Claim 16; Page 79; 82pp; English.

XX The present sequence represents a human potassium channel protein, termed

KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are

useful for identifying a compound that modulates its activity. The KCNB

polypeptide and nucleic acid are useful for detecting cancer cells in

biological samples. The inhibitor of the potassium channel polypeptide is

useful for inhibiting proliferation of a cancer cell and for treating a

potassium channel-associated disorder. The KCNB nucleic acids, proteins,

and/or antibodies are useful in the diagnosis or prognosis, or treatment

CC of diseases associated with altered KCNB activity or expression. Such  
CC diseases are cancer, brain associated disorders (such as epilepsy,  
CC Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis,  
CC migraine), psychiatric disorders (such as depression, schizophrenia,  
CC bipolar disease) and diseases related to the heart (such as  
CC arrhythmias), diseases related to pancreas (such as pancreatitis and  
CC diabetes)  
XX  
SQ Sequence 374 AA;

Query Match 54.7%; Score 1116; DB 4; Length 374;  
Best Local Similarity 59.0%; Pred. No. 3.5e-112;  
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Qy 1 MKQNVRTALIVCTTFTYLLVGAADVDALESEPELIERORLELRQBELRARNYLSQGGYE 60  
Db 1 MKQNVRTSLIVCTTFTYLLVGAADVDALESDHEMEEEKLKAEEIRIKGYNISSDYR 60  
Qy 61 ELERVVLRLKPKHAGVQWRFAGSFYFAITVITTTIGYHAAFGTDGKVFQCMFYAVLGIPL 120  
Db 61 QLELVILQSEPHRAGVQWKFAAGFYFAITVITTTIGYHAAFGTDAGKAFCMFYAVLGIPL 120  
Qy 121 TLVMFQSLGERINTLVYLLHRAKKGLGMRRADVSMANMVLIGFFSCITSLCIGAAAFSH 180  
Db 121 TLVMFQSLGERMNTFVYLLKRIKKCGMRNTDVS MENMVTGFFSCMGTLCIGAAAFSQ 180  
Qy 181 YEHWTFFQAYYYCIFTITTTIGFGDYVALQKDQALQTOPOVYVAFSVVYLLTGLTVIGAFNL 240  
Db 181 CEWSFFHAYYYCIFTITTTIGFGDYVALQKDQALQKPLVYVAFSFMVILVGLTVIGAFNL 240  
Qy 241 LVLRFMTWNAEDKRAEHRALTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNVY 300  
Db 241 LVLRFMTWNSDEDRDAERASL-----AGNRNSMVIHPEPRPS-----RPRY 286  
Qy 301 -AEVLHFQSMCCLWYKSRKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359  
Db 287 KADVPDLQSVCSCTCYRSQD---YGRSVAPQNSFSAKLAPHYFHSYKIEISPSSTLK 343  
Qy 360 RCLCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394  
Db 344 NSLFP-----SPISSISPLHSFTDHQRLMKRRKSV 374

## RESULT 13

AAE13279

ID AAE13279 standard; protein; 374 AA.

XX AAE13279;

XX AAE13279;

XX 12-FEB-2002 (first entry)

XX Human transporters and ion channels (TRICH)-6.

XX Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;

XX diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;

XX cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;

XX neurological disorder; Alzheimer's disease; cataract; infertility;

XX Wilson's disease; schizophrenia; Grave's disease; Addison's disease;

XX Huntington's disease; multiple sclerosis; meningitis; hypotensive;

XX cardiac; noctropic; neuroprotective; neuroleptic; ophthalmological;

XX antithyroid; anticonvulsant; goitre; antiinflammatory.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1. .25

XX /label= Signal\_peptide

XX 26. .374

XX Protein

XX /note= "Human mature TRICH6 protein"

XX 225. .243

XX Domain

XX /label= Transmembrane\_domain

XX WO200177174-A2.

PN













```

Qy 230 TG-----LTVIGAFNLNLVVL-----RFMTWNAEDKKDAEH 260
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 LGLIAMLVVLETFCELHELKKFRKMFYVKKDKOBDQVH 292

RESULT 7
T25933
hypothetical protein C52B9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28933
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: Z20545
A:Accession: T28933
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-513 <NEL>
A:Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN0028; CESP:C52B9.6
A:Experimental source: strain Bristol N2; clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.6
A:Map position: X
A:Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 4
      Query Match 15.1%; Score 307.5; DB 2; Length 513;
      Best Local Similarity 23.6%; Pred. No. 9.1e-20;
      Matches 105; Conservative 56; Mismatches 139; Indels 145; Gaps 12
Qy 9 LALIVCTFTYLLVGAAVFDALSEPEL-----IERORLELRQQLRARNYLSGGYEEL 62
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 VGLVILLFLYLIAGAFRLRYLEAPKELESDNRISREAFNAIQEY-----PEQL 112
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 63 ERVVLRL-----KPHKAGVQWRFAGSFYFAITVITTI----- 94
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 VKMFMQAYRNQFITAKHLNKTREDEVLWTFPNSMFFAATVITTVQKNRSGNRVFSR 172
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 95 GYGHAAAPSTDGGKVFQCMFYALLGIPLTVMVFQSLGERINTLVYLLHRAKKGLGMR----- 150
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 GYGNLVPITVTGRVACIIIFALLGIPLLVTIADIGKLFSELSY-LVRSYRGFKKLRQQ 231
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 151 -----RADVSNANMVLIGFF 165
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 SKKITSYRSQSQRSSSVMSGSKAGSMNLHDDSDSEDSAGDELRIPIVFMVLVLVLLAY- 290
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 166 SCISTLCIGAAASHVEHHTFFQAYYCFITLTIGGDYVALQDQALQTOPOYVAFSP 225
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 -----TAIGGLFQSWHEHLYFEAFYFCFITMATVGFQDIV-----PNEQYVYVFTM 337
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 226 VYILTGLTVIGAFNLNV-----VLRFMTWNAEDKKDAEHRAILLTRNGOAGGGGGGSA 279
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 338 AYIIFGLSLATMCIDLAGTYIRKIHVLTGTMEDAK-----GAVMTGLQGEH 385
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 280 HTTDTASTASAAAGGGGFRNRYAELHFQ-----SMCSCLMYKSRKQLQYSIPM----- 327
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 386 LLKHTGIEVKTAGGKLQVRGAVLSSKEARELGMSYLLQFNQHKNVLYEPLTGNLAKV 445
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 328 -----IIPRDLSTSDTCVEQSHS 345
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 446 VKEANIKILPDDITEKDGYIVQNKs 470
      |||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25392
R:Lloyd, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20027

```



R:Gattung, S.; Wu, X.  
submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid F20A1.  
A:Reference number: Z20726  
A:Accession: T30037  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1539 <GAT>  
A:Cross-references: UNIPROT:Q19611; EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1  
A:Experimental source: strain Bristol N2; clone F20A1  
C:Genetics:  
A:Map position: 5  
A:Introns: 13/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110/3  
Query Match 13.1%; Score 268; DB 2; Length 1539;  
Best Local Similarity 24.6%; Pred. No. 1.3e-15;  
Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps 13;  
QY 8 TLALIVCTTYLLVGAADFALSEPELIERQ-----RLRQQLERA-RYNLSQGG 58  
DB 88 TPKLLIIIGLSPIGAHIFWLEVPDLEAREDPHQRIAREVMVNLRAIFYDNREDR 147  
QY 59 YEELERVVLRKPKHAGVQ-----WRFAGSFYFAITVTTIGYGHAASTDDGKVFQM 111  
DB 148 ERWRKHAULKFE-EDIGLEBPVETVTFWMSFLYAGTIFTTIGYGNIACTKTRAGQIATM 206  
QY 112 FYALGIGIPTLVNFQSL-----GERI----- 132  
DB 207 VFAVGIPIMLVNLTSLNNFLKWKILITNGVSDMTLYIGVRLGITVIRQDEVQKRLRYT 266  
QY 133 ----NTLVRVLL--HRAKGLGHRADVSMNM-----VLIGFFSCISTL 171  
DB 267 KLAKTMKRWKLSKHGAPSAISSEENLNSTPEDDEBEETHQDPVPLSTLIATVAMI 326  
QY 172 CIGMAAFSHYHWTFFQAYYCFITLTITGFDYVALQDQALQTOPOQVVAFFVILNG 231  
DB 327 ILSSAAVFCUFEDWTFTFTSYFCISLTITGLGD-----VTPANPEYMIATFGVVIWG 378  
QY 232 LTVIGAFNLVLRFMNMADEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAA 291  
DB 379 LSLMTVICIDVQLKLAQTM-----ALLOKLTEYWEAVKSG-----DPNAAASAMWA 425  
QY 292 GGGG-----FRNYAEVL-HFQSMCS 311  
DB 426 GFQGRAKFLMPLISKNEGAKVMDKFKQDCS 455  
RESULT 12  
T21598  
hypothetical protein F31D4.7 - Caenorhabditis elegans.  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21598  
R:Morimore, B.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19447  
A:Accession: T21598  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-443 <WIL>  
A:Cross-references: UNIPROT:O45422; EMBL:Z92832; PIDN:CA07375.1; GSPDB:GN00023; CESP:F31D4  
A:Experimental source: clone F31D4  
C:Genetics:  
A:Gene: CESP:F31D4.7  
A:Map position: 5  
A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3  
Query Match 12.8%; Score 262; DB 2; Length 443;  
Best Local Similarity 25.0%; Pred. No. 1e-15;  
Matches 78; Conservative 55; Mismatches 113; Indels 66; Gaps 9;  
QY 11 LIVCTTYLLVGAADFALSEPELIERQ-----RLRQQLERA-RYNLSQGG 56

DB 17 LLIIVLIYICISGLVFWLIEEYQSELDRDAWOKHNNRTARVDAMKKIFNNSDYLIYI 76  
QY 57 -----GGYEELERVVLRKPKHAGVQWRFAGSFYFAITVTTIGYGHAA 100  
DB 77 KGNTSRLTFTTFIEELGSYEN---QLGVKWSQQRMDWDFWNAVLPAFTICTTIGYGHIV 132  
QY 101 PSTDGGKVFCEYALLGIPLTIVMQSISGERINTLVRYLLHRAKGL----- 147  
DB 133 PMTDAGRLMTIFALFGIPLMLLVLLVQDFGLKLTITMKFPWFQTKRLMRMRMCCTKQPIE 192  
QY 148 -----GMRRADVSMNMVWL-IGFFSCISTLCIGAAAFSHYH-WTFFQAYYCFITLT 199  
DB 193 EMKEIERQERHDDIDFIDPLPGVIALIVTWIFICFVLSVWDHNTLLESFPPFFTSLSLT 252  
QY 200 IGFGDYVALQDQALQTOPOQVVAFFVILGTIGVAFNLVLRFMFMT---MNADEK 256  
DB 253 VGLGDLV-----PSSPRLITWFGFILVGLSLVSMVINLLOAKMKSTYEAGRNDK 304  
QY 257 DAHRALLTRNG 268  
DB 305 PHIQTLPTSLG 316  
RESULT 13  
T13807  
potassium channel protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: T13807  
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pauech, M.H.  
Proc. Natl. Acad. Sci. U.S.A. 93, 13258-13261, 1996  
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila  
A:Reference number: Z17770; MUID:97075152; PMID:8917578  
A:Accession: T13807  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1001 <GOL>  
A:Cross-references: UNIPROT:Q94526; EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AA669  
C:Genetics:  
A:Gene: ORK1  
A:Cross-references: FlyBase:FBgn0017561  
A:Map position: 1  
Query Match 12.8%; Score 261.5; DB 2; Length 1001;  
Best Local Similarity 25.0%; Pred. No. 3e-15;  
Matches 69; Conservative 65; Mismatches 107; Indels 35; Gaps 8;  
QY 7 RTALIVCTTYLLVGAADFALSEPELIERQELRQQLERARYNLSQGGYEEL----- 62  
DB 5 RWILLIFVYSYLMFGAAIYTHIEGEEKIS-----RAEQKAKAIATINEYLLEELGDKN 58  
QY 63 ----ERVVLR-----KP-----HKAGVQWRFAGSFYFAITVTTIGYGHAASTDDG 106  
DB 59 TTTQDEILQISDYCDKVPVLTPTDTPYTWTFHAFFAFTVCTVGYGNISPTTFAG 118  
QY 107 KVFCEYALLGIPLTIVMQSISGERINTLVRYLLHRAK-----GLGMRRADVSMNMVWL 161  
DB 119 RMIMIAVSIGIPVNGILFAGLGEYFGRTFEAIYRKYKYSTDMHYVPPQLGLITTV 178  
QY 162 IGFFSCIST-LCIGAAAFSHYHWTFFQAYYCFITLTITIGFDYV-ALQKDQALQTOPO 219  
DB 179 IALIFGIALFLLLPSVTFENPYSISLYSYVTTTTTIGFDYVPTFGANQPKFEGGW 238  
QY 220 VVAFFSVVILGTIGVAFNLVLRFMFMTMNADEK 255  
DB 239 FVYQIFVIVWFIFSLGYL--VMIMFITRGLQSKK 272  
RESULT 14  
S44635  
f22b7.7 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

```

304 -NTISACVYITILEPNWSFLDSFYFCLVSLLLTVGFGD-----LHPDVGIVEYMLCS 351
Db
Qy      225 FVYILTGL 232
      ||: || ||
Db      352 IVFIFIGL 359

Search completed: July 13, 2005, 08:45:43
Job time : 21.7368 secs
```

Search completed: July 13, 2005, 08:45:43  
Job time : 21.7368 secs

A;Residues: I-42 / <WILS  
A:Cross-references: UNIPROT:O23386; EMBL:Z70038; PIDN:CAA93881.1; GSPDB:GN00020; CESP:ZK

Query Match 12.7%; Score 258.5; DB 2; Length 427;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005: Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 86.5115 Seconds  
(without alignments)  
1759.475 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MRQNVRTALIVCTFYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	9 US-09-939-484-4	Sequence 4, Appli
2	2042	100.0	394	9 US-09-939-483-4	Sequence 4, Appli
3	2042	100.0	394	9 US-09-798-584-15	Sequence 15, Appl
4	2042	100.0	394	14 US-10-146-733-17	Sequence 17, Appl
5	2042	100.0	394	14 US-10-146-733-18	Sequence 18, Appl
6	2042	100.0	395	14 US-10-146-733-8	Sequence 8, Appli
7	1850.5	90.6	412	14 US-10-146-733-9	Sequence 9, Appli
8	1819	89.1	405	9 US-09-939-484-5	Sequence 5, Appli
9	1819	89.1	405	9 US-09-939-483-5	Sequence 5, Appli
10	1278	62.6	258	9 US-09-746-491-61	Sequence 61, Appl
11	1224	59.9	312	8 US-08-816-011-55	Sequence 55, Appl

Query Match 100.0%; Score 2042; DB 9; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.4e-180;

12	1224	59.9	312	17	US-10-870-492-55	Sequence 55, Appl
13	1154	56.5	233	15	US-10-459-190-15	Sequence 15, Appl
14	1116	54.7	374	9	US-09-798-584-1	Sequence 1, Appli
15	1116	54.7	374	14	US-10-146-733-41	Sequence 41, Appl
16	1116	54.7	374	15	US-10-257-022-6	Sequence 6, Appli
17	1116	54.7	374	15	US-10-074-978A-194	Sequence 194, App
18	1077.5	52.8	387	15	US-10-074-978A-195	Sequence 195, App
19	1069.5	52.4	365	9	US-09-746-491-60	Sequence 60, Appl
20	846	41.4	330	9	US-09-746-491-59	Sequence 59, Appl
21	846	41.4	330	15	US-10-173-999-42	Sequence 42, Appl
22	846	41.4	330	15	US-10-074-978A-192	Sequence 192, App
23	846	41.4	330	15	US-10-074-978A-193	Sequence 193, App
24	846	41.4	400	14	US-10-146-733-5	Sequence 5, Appli
25	838	41.0	330	9	US-09-746-491-58	Sequence 58, Appl
26	838	41.0	330	15	US-10-074-978A-191	Sequence 191, App
27	838	41.0	330	15	US-10-336-472-76	Sequence 76, Appl
28	838	41.0	393	9	US-09-746-491-22	Sequence 22, Appl
29	838	41.0	400	14	US-10-146-733-2	Sequence 2, Appli
30	838	41.0	400	15	US-10-257-022-13	Sequence 13, Appl
31	774	37.9	279	9	US-09-864-761-34389	Sequence 34389, A
32	619	30.3	212	15	US-10-074-978A-24	Sequence 24, Appl
33	507.5	24.9	179	15	US-10-424-599-216417	Sequence 216417,
34	370	18.1	370	9	US-09-939-484-8	Sequence 8, Appli
35	370	18.1	370	9	US-09-939-483-8	Sequence 8, Appli
36	369	18.1	411	9	US-09-828-746-6	Sequence 6, Appli
37	366.5	17.9	295	16	US-10-343-903-8	Sequence 8, Appli
38	366	17.9	487	17	US-10-461-862-129	Sequence 129, App
39	364	17.8	422	16	US-10-349-528-20	Sequence 20, Appl
40	364	17.8	426	8	US-08-816-011-45	Sequence 45, Appl
41	364	17.8	426	17	US-10-870-492-45	Sequence 45, Appl
42	363	17.8	411	9	US-09-828-746-2	Sequence 2, Appli
43	363	17.8	411	11	US-09-892-360-18	Sequence 18, Appl
44	363	17.8	411	14	US-10-121-746-83	Sequence 83, Appl
45	363	17.8	411	16	US-10-745-210-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-939-484-4  
; Sequence 4, Application US/09939484  
; Patent No. US20020032322A1  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 1201-CIP-DIV-00  
; CURRENT APPLICATION NUMBER: US/09/939,484  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 09/144,914  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 08/749,816  
; PRIOR FILING DATE: 1996-11-15  
; PRIOR APPLICATION NUMBER: 60/095,234  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: FR 96/01565  
; PRIOR FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; TYPE: PRT  
; LENGTH: 394  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TASK  
US-09-939-484-4

Matches	394;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;																																											
Qy	1	MKQNVRTLALI	VCTFTYLLVGA	VPAL	SEPE	LI	ERQLE	RQQLR	ARYNLS	QGGYE	60																																									
Db	1	MKQNVRTLALI	VCTFTYLLVGA	VPAL	SEPE	LI	ERQLE	RQQLR	ARYNLS	QGGYE	60																																									
Qy	61	ELERVVLR	LKPHKAGV	QWR	FAGS	FYP	PAI	TV	TTTIGY	GHAAP	STDG	GKVFCM	FYALL	GIPL	120																																					
Db	61	ELERVVLR	LKPHKAGV	QWR	FAGS	FYP	PAI	TV	TTTIGY	GHAAP	STDG	GKVFCM	FYALL	GIPL	120																																					
Qy	121	TLVMFQSL	GERINT	LV	RYLLH	RKAG	GLG	MRR	ADY	SMAN	MV	LIG	FF	SCIST	TL	CIG	AAAF	SH	180																																	
Db	121	TLVMFQSL	GERINT	LV	RYLLH	RKAG	GLG	MRR	ADY	SMAN	MV	LIG	FF	SCIST	TL	CIG	AAAF	SH	180																																	
Qy	181	YEHWTF	FQAYYY	CE	IT	LT	TTIG	F	GDY	VAL	OK	D	Q	AL	Q	T	Q	Y	V	A	F	S	V	I	L	T	G	I	G	A	F	L	N	240																		
Db	181	YEHWTF	FQAYYY	CE	IT	LT	TTIG	F	GDY	VAL	OK	D	Q	AL	Q	T	Q	Y	V	A	F	S	V	I	L	T	G	I	G	A	F	L	N	240																		
Qy	241	LVVLR	FMT	MNA	DE	KR	DA	EH	R	AL	T	R	N	G	Q	G	G	G	G	G	S	A	H	T	T	D	T	A	S	T	A	A	A	G	G	G	F	R	N	V	300											
Db	241	LVVLR	FMT	MNA	DE	KR	DA	EH	R	AL	T	R	N	G	Q	G	G	G	G	G	S	A	H	T	T	D	T	A	S	T	A	A	A	G	G	G	F	R	N	V	300											
Qy	301	AEVLH	FQ	SM	C	S	C	L	Y	K	S	R	E	K	L	Q	Y	S	I	P	M	I	I	P	R	D	L	S	T	S	T	C	V	E	Q	S	H	S	S	P	G	G	G	R	Y	S	D	T	S	R	R	360
Db	301	AEVLH	FQ	SM	C	S	C	L	Y	K	S	R	E	K	L	Q	Y	S	I	P	M	I	I	P	R	D	L	S	T	S	T	C	V	E	Q	S	H	S	S	P	G	G	G	R	Y	S	D	T	S	R	R	360
Qy	361	CLCSG	AP	R	S	A	I	S	S	V	S	T	G	L	H	S	L	S	T	F	R	G	L	M	K	R	A	S	S	V	394																					
Db	361	CLCSG	AP	R	S	A	I	S	S	V	S	T	G	L	H	S	L	S	T	F	R	G	L	M	K	R	A	S	S	V	394																					

## RESULT 2

```

US-09-939-483-4
; Sequence 4, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Leagee, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 03/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-4

```

Db	61	ELERVVLRLKPHKAGVQWRFAGSFYFAITVTITIGYCHAA PSTDGGKVFCMFVALLGCIPL	120
Qy	121	TLVMFQSLGERINTLVRYLLHRAKKGLMRRADVSMANMVLIGFFSCISTLCIGAAAFSH	180
Db	121	TLVMFQSLGERINTLVRYLLHRAKKGLMRRADVSMANMVLIGFFSCISTLCIGAAAFSH	180
Qy	181	YEHWTFFQAYYYCFITLTTTIGFGDYVALQKDQALQTPQVVAESFVYILTGLTVIGAFNL	240
Db	181	YEHWTFFQAYYYCFITLTTTIGFGDYVALQKDQALQTPQVVAESFVYILTGLTVIGAFNL	240
Qy	241	LVLRPMTWMAEDBKDAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFRNVY	300
Db	241	LVLRPMTWMAEDBKDAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFRNVY	300
Qy	301	AEVLHFQSMCSCLVWYKSREKLQYISIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTFSRR	360
Db	301	AEVLHFQSMCSCLVWYKSREKLQYISIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTFSRR	360
Qy	361	CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	394
Db	361	CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	394

RESULT 3

US-09-798-584-15

Sequence 15, Application US/09798584

Patent No. US20020102676A1

GENERAL INFORMATION:

APPLICANT: Mu, David

APPLICANT: Powers, Scott

APPLICANT: Tularik Inc.

TITLE OF INVENTION: KCNB: A No. US20020102676A1el Potassium Channel Protein

FILE REFERENCE: 018781-004010US

CURRENT APPLICATION NUMBER: US/09/798,584

CURRENT FILING DATE: 2001-03-03

PRIOR APPLICATION NUMBER: US 60/186,951

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin ver. 2.1

SEQ ID NO 15

LENGTH: 394

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human potassium channel KCNK3 (TASK1)

Query Match

Best Local Similarity 100.0%; Score 2042; DB 9; Length 394;

Marches 394: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

### RESULT 3

```

US-09-798-584-15
; Sequence 15, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A No. US20020102676A1el Potass
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human potassium channel KCNK3 (TASK1)
US-09-798-584-15

Query Match      100.0%; Score 2042; DB 9; Length
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indel

```



Db 301 AEVLHFQSMCCLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGRYSDTPSRR 360  
Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
RESULT 4  
US-10-146-733-17  
; Sequence 17, Application US/10146733  
; Publication No. US20030165891A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtie, Rory A.J.  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MNI-248  
; CURRENT APPLICATION NUMBER: US/10/146,733  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/185,938  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/515,520  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/518,866  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/195,993  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: US 60/199,799  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/233,537  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US 60/235,018  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/256,588  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-146-733-17  
Query Match 100.0%; Score 2042; DB 14; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.4e-180;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCRQNVRLALIVCTFTYLLVCAAVFDALSEPELIERORLELRQOELRARNLSQGGYE 60  
Db 1 MCRQNVRLALIVCTFTYLLVCAAVFDALSEPELIERORLELRQOELRARNLSQGGYE 60  
Qy 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAAAPSTDGKGKVFCMFYALLGIPL 120  
Db 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYGHAAAPSTDGKGKVFCMFYALLGIPL 120  
Qy 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRRAVDSNMANNVLIGFFSCISTLCIGAAAFSH 180  
Db 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRRAVDSNMANNVLIGFFSCISTLCIGAAAFSH 180  
Qy 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALQTOPOYVAFSFYIITGLTVIGAFLN 240  
Db 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALQTOPOYVAFSFYIITGLTVIGAFLN 240  
Qy 241 LVVLFPMTNWADKRAHRAKGLGMRRAVDSNMANNVLIGFFSCISTLCIGAAAFSH 300  
Db 241 LVVLFPMTNWADKRAHRAKGLGMRRAVDSNMANNVLIGFFSCISTLCIGAAAFSH 300  
Qy 301 AEVLHFQSMCCLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGRYSDTPSRR 360  
Db 301 AEVLHFQSMCCLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGRYSDTPSRR 360  
Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
RESULT 5  
US-10-146-733-18  
; Sequence 18, Application US/10146733  
; Publication No. US20030165891A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtie, Rory A.J.  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MNI-248  
; CURRENT APPLICATION NUMBER: US/10/146,733  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/185,938  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/515,520  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/518,866  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/195,993  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: US 60/199,799  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/233,537  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US 60/235,018  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/256,588  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/258,028  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 09/796,720  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 09/828,035  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 09/833,081  
; PRIOR FILING DATE: 2001-04-11

```
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-18

Query Match      100.0%; Score 2042; DB 14; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSQGGYE 60
Db 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSQGGYE 60

Qy 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120
Db 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120

Qy 121 TLVMPQSLGERINTLVRYLLHRACKGLGMRADVSMANNVLLIGFSPSCISTLCIGAAAFSH 180
Db 121 TLVMPQSLGERINTLVRYLLHRACKGLGMRADVSMANNVLLIGFSPSCISTLCIGAAAFSH 180

Qy 181 YEHWTFQAYYYCFITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 240
Db 181 YEHWTFQAYYYCFITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 240

Qy 241 LVVLFMTWNAEDEKRAHRLTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNYY 300
Db 241 LVVLFMTWNAEDEKRAHRLTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNYY 300

Qy 301 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360
Db 301 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360

Qy 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 6
US-10-146-733-8
; Sequence 8, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47615,
; TITLE OF INVENTION: NMMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
```

```
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-8

Query Match      100.0%; Score 2042; DB 14; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSQGGYE 60
Db 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSQGGYE 61

Qy 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120
Db 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 121

Qy 121 TLVMPQSLGERINTLVRYLLHRACKGLGMRADVSMANNVLLIGFSPSCISTLCIGAAAFSH 180
Db 121 TLVMPQSLGERINTLVRYLLHRACKGLGMRADVSMANNVLLIGFSPSCISTLCIGAAAFSH 181

Qy 181 YEHWTFQAYYYCFITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 240
Db 181 YEHWTFQAYYYCFITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 241

Qy 241 LVVLFMTWNAEDEKRAHRLTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNYY 300
Db 241 LVVLFMTWNAEDEKRAHRLTRNGQAGGGGGGSAHTTDTASSTAAGGGGFRNYY 301

Qy 301 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360
Db 301 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSPTPSRR 361

Qy 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 395
```



```
QY 244 LRFMTMNAEDEKRDADHALLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
Db 241 LRFMTMNAEDEKRDADHALLTHNGOAVGLGSLCCLSGLDGVRPRDPVTCAAAAGGVGV 300
QY 292 --GGGGRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGG 349
Db 301 GVGSGFRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEHSHSPGG 360
QY 350 GGRYSDTPSRCLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 GGRYSDTPSHPCLCGTQKRSIAISSVSTGLHSLAAPRGLMKRRSSV 405

RESULT 9
US-09-939-483-5
; Sequence 5, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-5

Query Match 89.1%; Score 1819; DB 9; Length 405;
Best Local Similarity 88.1%; Pred. No. 6.8e-160;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLQLELRARYNLSQGGYELE 63
Db 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLQLELRARYNLSQGGYELE 60
QY 64 RVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYALLGIPLTIV 123
Db 61 RVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYALLGIPLTIL 120
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADYVSMANNVLIGFVSCISTLCIGAAAFSHYEH 183
Db 121 MFQSLGERINTFVRYLLHRAKGLGMRHAEVSMANNVLIGFVSCISTLCIGAAAFSYER 180
QY 184 WTFPQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNLV 243
Db 181 WTFPQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNLV 240
QY 244 LRFMTMNAEDEKRDADHALLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
Db 241 LRFMTMNAEDEKRDADHALLTHNGOAVGLGSLCCLSGLDGVRPRDPVTCAAAAGGVGV 300
QY 292 --GGGGRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGG 349
Db 301 GVGSGFRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEHSHSPGG 360
```

```
QY 350 GGRYSDTPSRCLCGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 GGRYSDTPSHPCLCGTQKRSIAISSVSTGLHSLAAPRGLMKRRSSV 405

RESULT 10
US-09-746-491-61
; Sequence 61, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-746-491-61

Query Match 62.6%; Score 1278; DB 9; Length 258;
Best Local Similarity 96.1%; Pred. No. 5.7e-110;
Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKQNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLQLELRARYNLSQGGYE 60
Db 1 MKQNVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLQLELRARYNLSQGGYE 60
QY 61 ELERVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYALLGIP 120
Db 61 ELERVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYALLGIP 120
QY 121 TLVMPQSLGERINTLVRYLLHRAKGLGMRADYVSMANNVLIGFVSCISTLCIGAAAFSH 180
Db 121 TLVMPQSLGERINTFVRYLLHRAKGLGMRHAEVSMANNVLIGFVSCISTLCIGAAAFSY 180
QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAF 240
Db 181 YERWTFPQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAF 240

QY 241 LVVLRFTMTMNAEDEKRD 258
Db 241 LVVLRFTMTMNAEDEKRD 258
```

```
RESULT 11
US-08-816-011-55
; Sequence 55, Application US/08816011
; Publication No. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Fausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/816,011  
;; FILING DATE: 11-MAR-1997  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Matthews, Gale F.  
;; REGISTRATION NUMBER: 32,269  
;; REFERENCE/DOCKET NUMBER: 32,421-C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-683-2134  
;; TELEFAX: 201-683-4117  
;; INFORMATION FOR SEQ ID NO: 55:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 312 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-816-011-55

Query Match 59.9%; Score 1224; DB 8; Length 312;  
Best Local Similarity 83.1%; Pred. No. 7.4e-105;  
Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

QY 4 QNVRTLALIVCTFTYLLVGAAVFDALSEPELIERORLELRQQLRARNYLSGGYEEL 63  
DB 13 ENVRTLALIVCTFTYLLVGAAVFDALSEPEMIEORLELRQQLRARNYLSGGYEEL 72

QY 64 RVVRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGV---FCMFYALLGIPL 120  
DB 73 RVVRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPL 132

QY 121 TLVMSFSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180  
DB 133 TLVMSFSLGERINTSVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 192

QY 181 YEHWTFFQAYYCFITLTITIGFDYVALQDQALQTPQYVAFSFYVILTLTVIG--AF 238  
DB 193 YERWTFQAYYCFITLTITIGFDYVALQDQALQTPQYVAFSASCTSSRAHGHRF 249

QY 239 LNLVLRFTWMADEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAA 290  
DB 250 LNLVLRFTWMADEKRAEHRALLTHNGQAVLGSLGSLSDGVRPRDPTVCAAA 309

QY 291 A 291  
DB 310 A 310

RESULT 12  
US-10-870-492-55  
; Sequence 55, Application US/10870492  
; Publication No. US20050032165A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUSCH, MARK H.  
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
; AND METHODS OF USING SAME  
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/10/870,492  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/503,849  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/816,011  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR APPLICATION NUMBER: PCT/US95/14364  
; PRIOR FILING DATE: 1995-10-25  
; PRIOR APPLICATION NUMBER: 07/332,312  
; PRIOR FILING DATE: 1994-10-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-10-870-492-55

Query Match 59.9%; Score 1224; DB 17; Length 312;  
Best Local Similarity 83.1%; Pred. No. 7.4e-105;  
Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

QY 4 QNVRTLALIVCTFTYLLVGAAVFDALSEPELIERORLELRQQLRARNYLSGGYEEL 63  
DB 13 ENVRTLALIVCTFTYLLVGAAVFDALSEPEMIEORLELRQQLRARNYLSGGYEEL 72

QY 64 RVVRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGV---FCMFYALLGIPL 120  
DB 73 RVVRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPL 132

QY 121 TLVMSFSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180  
DB 133 TLVMSFSLGERINTSVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 192

QY 181 YEHWTFFQAYYCFITLTITIGFDYVALQDQALQTPQYVAFSFYVILTLTVIG--AF 238  
DB 193 YERWTFQAYYCFITLTITIGFDYVALQDQALQTPQYVAFSASCTSSRAHGHRF 249

QY 239 LNLVLRFTWMADEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAA 290  
DB 250 LNLVLRFTWMADEKRAEHRALLTHNGQAVLGSLGSLSDGVRPRDPTVCAAA 309

QY 291 A 291  
DB 310 A 310

RESULT 13  
US-10-459-190-15  
; Sequence 15, Application US/10459190  
; Publication No. US20040072216A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Jeffrey D.  
; APPLICANT: Palma, John F.  
; APPLICANT: Schweitzer, Anthony C.  
; APPLICANT: Blume, John E.  
; APPLICANT: Metabolex, Inc.  
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing  
; Diabetic  
; FILE REFERENCE: 016325-0082100S  
; CURRENT APPLICATION NUMBER: US/10/459,190  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/387,642  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: transmembrane (TM) and pore domains of mouse  
; OTHER INFORMATION: TWIK-related acid-sensitive potassium channel 1  
; OTHER INFORMATION: (TASK-1)  
US-10-459-190-15

Query Match 56.5%; Score 1154; DB 15; Length 233;  
Best Local Similarity 95.7%; Pred. No. 1.6e-98;  
Matches 223; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 RTLALIVCTFTYLLVGAAVFDALSEPELIERORLELRQQLRARNYLSGGYEELRVV 66  
DB 1 RTLALIVCTFTYLLVGAAVFDALSEPEMIEORLELRQQLRARNYLSGGYEELRVV 60

QY 67 LRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 126  
DB 61 LRLKPKHAGVQWRFGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 120

QY 127 SLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSHYEHWT 186

Db 121 SGERINTFVRLHRAKGLGMRHAEVSMANVILGFCVSCISTLCIGAAAFSYYERTWF 180  
Qy 187 FOAYYYCFTITLTIGFDYVALQKQALOTQPOYVAFSFVYILTLGLTVIGAF 239  
Db 181 FOAYYYCFTITLTIGFDYVALQKQALOTQPOYVAFSFVYILTLGLTVIGAF 233

RESULT 14  
US-09-798-584-1  
; Sequence 1, Application US/09798584  
; Patent No. US20020102676A1  
; GENERAL INFORMATION:  
; APPLICANT: Mu, David  
; APPLICANT: Powers, Scott  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: KCNB: A No. US20020102676A1e1 Potassium Channel Protein  
; FILE REFERENCE: 018781-004010US  
; CURRENT APPLICATION NUMBER: US/09/798,584  
; CURRENT FILING DATE: 2001-03-03  
; PRIOR APPLICATION NUMBER: US 60/186,951  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)  
US-09-798-584-1

Query Match 54.7%; Score 1116; DB 9; Length 374;  
Best Local Similarity 59.0%; Pred. No. 9.7e-95;  
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
Qy 1 MKRQVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSQGYE 60  
Db 1 MKRQVRLSLIVCTFTYLLVGAADFDALESDHEMREKKAERIRKGNYSSEYR 60  
Qy 61 ELERVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVCFCMFYALLGIPL 120  
Db 61 QLEVLQSEPHRAGVQWKFGAGSFYFAITVTITIGYHAAAPSTDGAKAFCMFYAVLGIPL 120  
Qy 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVILGFSCISTLCIGAAAFSH 180  
Db 121 TLVVFQSLGERMNTFVRYLLKRIKCCGMRNTDVSMNNVTGVFFSCMTLCIGAAAFSQ 180  
Qy 181 YEHWTFFQAYYYCFTITLTIGFDYVALQKQALOTQPOYVAFSFVYILTLGLTVIGAF 240  
Db 181 CEWNSFFHAYYYCFTITLTIGFDYVALQKQALOTKALQKPLVYAFSPWYILVGLTVIGAF 240  
Qy 241 LVVLRPMTNABDEKRDABHALLTRNGOAGGGGGGSAHTTDTASSTAAGGGGRNVY 300  
Db 241 LVVLRFLTNSEDERDABERASL-----AGNRSMVTHIPEERPS-----RPRY 286  
Qy 301 -REVLFHFSQCMCLWYKSEKLOYSTPMIIPDLSTSDTCVZQSHSPGGGRYSDTSR 359  
Db 287 KADVPDQVCSCTCYRSQD---YGRSVAPQNSFSAKLAPHYFHSISYKTEISPSTLK 343  
Qy 360 RCLCSGAPSAISSVSTGLHLSLSTRGLMKRSSV 394  
Db 344 NSLFP-----SPISSISPLHLSHTDQRLMKRKS 374

RESULT 15  
US-10-146-733-41  
; Sequence 41, Application US/10146733  
; Publication No. US20030165891A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Silos-Santiago, Inmaculada

; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,  
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES  
; FILE REFERENCE: MNI-248  
; CURRENT APPLICATION NUMBER: US/10/146,733  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/185,938  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/515,520  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: US 09/518,866  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: US 60/195,734  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/195,993  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: US 60/199,799  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/233,537  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US 60/235,018  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/235,059  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US 60/256,240  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/256,588  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/258,028  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 09/796,720  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 09/828,035  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 09/833,081  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 09/843,128  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: US 09/957,683  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: US 09/964,252  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 09/964,256  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 10/024,623  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-146-733-41  
Query Match 54.7%; Score 1116; DB 14; Length 374;  
Best Local Similarity 59.0%; Pred. No. 9.7e-95;  
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
Qy 1 MKRQVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSQGYE 60  
Db 1 MKRQVRLSLIVCTFTYLLVGAADFDALESDHEMREKKAERIRKGNYSSEYR 60  
Qy 61 ELERVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVCFCMFYALLGIPL 120  
Db 61 QLEVLQSEPHRAGVQWKFGAGSFYFAITVTITIGYHAAAPSTDGAKAFCMFYAVLGIPL 120  
Qy 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVILGFSCISTLCIGAAAFSH 180  
Db 121 TLVVFQSLGERMNTFVRYLLKRIKCCGMRNTDVSMNNVTGVFFSCMTLCIGAAAFSQ 180  
Qy 181 YEHWTFFQAYYYCFTITLTIGFDYVALQKQALOTQPOYVAFSFVYILTLGLTVIGAF 240  
Db 181 CEWNSFFHAYYYCFTITLTIGFDYVALQKQALOTKALQKPLVYAFSPWYILVGLTVIGAF 240

```
QY 241 LVVLRPMWNAEDEKRDADHRALLTRNGQAGCGGGGSAHTTDTASSTAAGGGFRNVY 300
Db 241 LVVLRFLTMNSEDERDAERASL-----AGNRNSMVIHIPEEPRPS-----RPRY 286
QY 301 -AEVLHFQSMCCLWYKREKLOYSIPIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359
Db 287 KADVPLQVSCCTCYRSQP---YGGRSVAPQNSFSAKLAPHYFHSISYKIEISFSTLK 343
QY 360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 344 NSLFP----SPISSISPLHSFTDQRLMKRRKSV 374
```

Search completed: July 13, 2005, 09:07:02  
Job time : 87.5115 secs

**This Page Blank (uspio)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 25.273 Seconds  
(without alignments)  
1163.760 Million cell updates/sec

Title: US-09-503-089A-5  
Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRGIMKRRSV 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	3	US-09-144-914-4
2	1819	89.1	405	3	US-09-144-914-5
3	1116	54.7	388	4	US-09-949-016-7631
4	773	37.9	408	4	US-09-362-842-12
5	379	18.6	361	4	US-09-362-842-14
6	370	18.1	370	3	US-09-144-914-8
7	369	18.1	411	3	US-09-236-080-6
8	363	17.8	411	3	US-09-236-080-2
9	363	17.8	411	3	US-09-336-643A-83
10	349.5	17.1	538	4	US-09-949-016-7001
11	349.5	17.1	558	4	US-09-949-016-7368
12	329.5	16.1	393	4	US-09-432-470-2
13	329.5	16.1	393	4	US-09-432-470-4
14	329.5	16.1	419	4	US-09-949-016-6913
15	329.5	16.1	440	4	US-09-949-016-7809
16	320.5	15.7	336	3	US-08-749-816-2
17	320.5	15.7	336	3	US-09-144-914-2
18	319	15.6	499	4	US-09-561-763-2
19	319	15.6	499	4	US-09-431-367B-2
20	312	15.3	146	4	US-09-362-842-69
21	312	15.3	146	4	US-09-270-767-31685
22	295.5	14.5	313	3	US-09-336-643A-81
23	295.5	14.5	313	4	US-09-561-763-8
24	295.5	14.5	313	4	US-09-431-367B-8
25	294.5	14.4	332	4	US-09-561-763-5
26	294.5	14.4	332	4	US-09-431-367B-5
27	278.5	13.6	995	4	US-09-362-842-2

28	253	12.4	336	1	US-08-332-312-4	Sequence 4, Appli
29	251.5	12.3	401	4	US-09-561-763-11	Sequence 11, Appl
30	251.5	12.3	401	4	US-09-431-367B-11	Sequence 11, Appl
31	245.5	12.0	395	4	US-09-362-842-6	Sequence 6, Appli
32	231.5	11.3	618	1	US-08-332-312-2	Sequence 2, Appli
33	221.5	10.8	257	4	US-09-949-016-6654	Sequence 6654, Ap
34	221.5	10.8	273	4	US-09-949-016-7794	Sequence 7794, Ap
35	212.5	10.4	730	4	US-09-362-842-4	Sequence 4, Appli
36	212.5	10.4	741	4	US-09-362-842-67	Sequence 67, Appl
37	212.5	10.4	741	4	US-09-270-767-45442	Sequence 45442, A
38	190.5	9.3	383	3	US-08-749-816-4	Sequence 4, Appli
39	190.5	9.3	383	3	US-09-144-914-7	Sequence 7, Appli
40	176.5	8.6	107	3	US-09-236-080-4	Sequence 4, Appli
41	156.5	7.7	1153	4	US-09-362-842-8	Sequence 8, Appli
42	156	7.6	347	3	US-08-749-816-3	Sequence 3, Appli
43	156	7.6	347	3	US-09-144-914-6	Sequence 6, Appli
44	147.5	7.2	132	4	US-09-362-842-10	Sequence 10, Appl
45	131.5	6.4	646	3	US-09-336-643A-10	Sequence 10, Appl

## ALIGNMENTS

## RESULT 1

US-09-144-914-4  
; Sequence 4, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989 6705CJP  
; CURRENT APPLICATION NUMBER: US/09/144,914  
; CURRENT FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749,816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095,234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TASK  
US-09-144-914-4

Query Match 100.0%; Score 2042; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 7.8e-217;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLROQLRARNLSOGGYE 60  
DB 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLROQLRARNLSOGGYE 60  
  
QY 61 ELERVVLRLKPKHAGVQWRFGAGSYFAITVITIGYHAAAPSTDGKVFQCMFYALIGIPL 120  
DB 61 ELERVVLRLKPKHAGVQWRFGAGSYFAITVITIGYHAAAPSTDGKVFQCMFYALIGIPL 120  
  
QY 121 TLVMPQSLGERINTLVRYLLHRKGLGNRRADVSMMANNVLIQGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPQSLGERINTLVRYLLHRKGLGNRRADVSMMANNVLIQGFSCISTLCIGAAAFSH 180  
  
QY 181 YEHWTFFQAYYYCFITLTIGTGDVVALQKQALQTOPOYVAFSFWITLTGTVTIGAFUN 240  
DB 181 YEHWTFFQAYYYCFITLTIGTGDVVALQKQALQTOPOYVAFSFWITLTGTVTIGAFUN 240

```
Qy 241 LVVLRFTMNAEDEKRDHALLTRNGOAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Db 241 LVVLRFTMNAEDEKRDHALLTRNGOAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Qy 301 AEVLHFQSMCWLKYKREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 360
Db 301 AEVLHFQSMCWLKYKREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 360
Qy 361 CLCSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394
Db 361 CLCSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394

RESULT 2
US-09-144-914-5
; Sequence 5, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-5

Query Match 89.1%; Score 1819; DB 3; Length 405;
Best Local Similarity 88.1%; Pred. No. 3.6e-192; Mismatches 25; Indels 14; Gaps 2;
Matches 357; Conservative 9;

Qy 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSOGGYEEL 63
Db 1 ENVRTALIVCTFTYLLVGAADFDALESEPEMIEHQRLERQLELRARYNLSOGGYEEL 60
Qy 64 RVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPLTIV 123
Db 61 RVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPLTII 120
Qy 124 MFQSLGERINTLVRYLLHRAKGLGMRADYSMMANNVLIGFSCISTLCIGAAAFSHYEH 183
Db 121 MFQSLGERINTFVRYLLHRAKGLGMRADYSMMANNVLIGFVSCISTLCIGAAAFSYER 180
Qy 184 WTFQAYYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNLV 243
Db 181 WTFQAYYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNLV 240
Qy 244 LRFMTMNAEDEKRDHALLTRNGOAGGGG-----GGSAHTTDTASSTAA----- 291
Db 241 LRFMTMNAEDEKRDHALLTRNGOAVGLGLSLCSGLSLGDPVRPRDPVTCAAAAGGVGV 300
Qy 292 --GGGGRNVVAVLHFMSCSLWYKREKLQYSIPMIIPRDLSTSDTCVEQSHSPGG 349
Db 301 GVGSGFRNVVAVLHFMSCSLWYKREKLQYSIPMIIPRDLSTSDTCVEHSHSPGG 360
Qy 350 GGRYSDTPSRRLCLSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394
Db 350 GGRYSDTPSRRLCLSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394
```

```
Db 361 GGRYSDTPSRRLCLSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 405

RESULT 3
US-09-949-016-7631
; Sequence 7631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7631
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7631

Query Match 54.7%; Score 1116; DB 4; Length 388;
Best Local Similarity 59.0%; Pred. No. 1.7e-114;
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Qy 1 MKRQNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSOGGYE 60
Db 15 MKRQNVRTLALIVCTFTYLLVGAADFDALESDHEMREBEKKAKEIRIKGKTNISSEYR 74
Qy 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIP 120
Db 75 QLELVILQSEPHRAGVQWKFGSFYFAITVTITIGYHAAAPGTDAGKAFYFVAVLGIPL 134
Qy 121 TLVMPQSLGERINTLVRYLLHRAKGLGMRADYSMMANNVLIGFSCISTLCIGAAAFSH 180
Db 135 TLVMPQSLGERINTFVRYLLKRIKCCGMRNTDYSMMNNVTVGFPSCMTLCIGAAAFSQ 194
Qy 181 YEHTFQAYYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNL 240
Db 195 CEWSFHYAYYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILVGLTVIGAFNL 254
Qy 241 LVVLRFTMNAEDEKRDHALLTRNGOAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Db 255 LVVLRFTMNAEDEKRDHALLTRNGOAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Qy 301 -AEVLHFQSMCWLKYKREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359
Db 301 KADVPDLQSVCSCTCYRSQD---YGGRSVAPQNSFSAKLAPHYFHSYKIEISPSFLK 357
Qy 360 RCLCSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394
Db 358 NSLFP-----SPISLSPLGHSFTDQRLMKRRKSV 388

RESULT 4
US-09-362-842-12
; Sequence 12, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; TITLE OF INVENTION: CHANNELS AND METHODS OF USE
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
```

```
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-362-842-12

Query Match 37.9%; Score 773; DB 4; Length 408;
Best Local Similarity 43.6%; Pred. No. 1.5e-76;
Matches 164; Conservative 66; Mismatches 82; Indels 64; Gaps 8;

QY 1 MKQNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGYE 60
Db 1 MKQNVRTISLIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGYE 60
QY 61 ELERVVLRLKPKAGVQWRGAGSYFAITVITIGYGHAAAPSTDDGKVFQCFMVALGIPL 120
Db 61 VMTVVVLKSSHKAGQWQKFTGAPYATVITIGYGHSTPSTVGGKLFMCAIVGIPL 120
QY 121 TLVMSFQSLGERINTLVRYLLHRAKKGGLGMRADYSMMANMVLIGFPFSCISTLCI--GAAAF 178
Db 121 GLVMFQSIGERVNRLSSVYIKAVRSSLRCKRTVASEVDLICV--VTLSSTIAGGAAP 178
QY 179 SHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQTOPOYVAFSFFVYILTLGLTVIGAF 238
Db 179 SKFEGSYFDSYVYCFITLTITIGFDYVALQKQALQTOPOYVAFSFFVYILTLGLTVIGAF 238
QY 239 LNLVLRFTMTNADEKRDRAHRL-----LTFNGOAGGGGGGSHHTDTTA 285
Db 239 LNLVLRFTMTNEDERRD-EAQMQLQAVKLEGDVITSNGSLSGYEGHDQSLSNGS 297
QY 286 SSTAAGGGGFRNVYAEVLHFQSCSC-----LWYKSRK-- 320
Db 298 -----NISMSCHCICLNGNRHKKSNLEKNDANQYKLRQST 338
QY 321 -LOYSIPMIIP-RDLS 334
Db 339 HIRHLLPEVVMQDLN 354

RESULT 5
US-09-362-842-14
; Sequence 14, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
US-09-362-842-14

Query Match 18.6%; Score 379; DB 4; Length 361;
Best Local Similarity 22.4%; Pred. No. 4.6e-33;
Matches 110; Conservative 52; Mismatches 113; Indels 64; Gaps 13;

QY 1 MKQNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGY 59
Db 39 MEKTSFRFSLYLPAFYFMFLCSGAAGVFSYFEAPERALRVKLGTAQVKFLVSNENVTADL 98
QY 60 EELERVVLRLKPKAGV-----QWRFGAGSYFAITVITIGYGHAAAPSTDDGKVF 109
Db 60 EELERVVLRLKPKAGV-----QWRFGAGSYFAITVITIGYGHAAAPSTDDGKVF 109

; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-362-842-12

Query Match 37.9%; Score 773; DB 4; Length 408;
Best Local Similarity 43.6%; Pred. No. 1.5e-76;
Matches 164; Conservative 66; Mismatches 82; Indels 64; Gaps 8;

QY 1 MKQNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGYE 60
Db 1 MKQNVRTISLIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGYE 60
QY 61 ELERVVLRLKPKAGVQWRGAGSYFAITVITIGYGHAAAPSTDDGKVFQCFMVALGIPL 120
Db 61 VMTVVVLKSSHKAGQWQKFTGAPYATVITIGYGHSTPSTVGGKLFMCAIVGIPL 120
QY 121 TLVMSFQSLGERINTLVRYLLHRAKKGGLGMRADYSMMANMVLIGFPFSCISTLCI--GAAAF 178
Db 121 GLVMFQSIGERVNRLSSVYIKAVRSSLRCKRTVASEVDLICV--VTLSSTIAGGAAP 178
QY 179 SHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQTOPOYVAFSFFVYILTLGLTVIGAF 238
Db 179 SKFEGSYFDSYVYCFITLTITIGFDYVALQKQALQTOPOYVAFSFFVYILTLGLTVIGAF 238
QY 239 LNLVLRFTMTNADEKRDRAHRL-----LTFNGOAGGGGGGSHHTDTTA 285
Db 239 LNLVLRFTMTNEDERRD-EAQMQLQAVKLEGDVITSNGSLSGYEGHDQSLSNGS 297
QY 286 SSTAAGGGGFRNVYAEVLHFQSCSC-----LWYKSRK-- 320
Db 298 -----NISMSCHCICLNGNRHKKSNLEKNDANQYKLRQST 338
QY 321 -LOYSIPMIIP-RDLS 334
Db 339 HIRHLLPEVVMQDLN 354

RESULT 5
US-09-362-842-14
; Sequence 14, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
US-09-362-842-14

Query Match 18.1%; Score 370; DB 3; Length 370;
Best Local Similarity 31.6%; Pred. No. 4.7e-32;
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKQNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQBELRARNLSQGGYE 60
Db 42 MKWKTSTYFLVW--VLYLIIGAFAKALEPQEQISQRTTIVIKQTFIAQAHACVNS--T 97
QY 61 ELERVVLRL-KPHKAGV-----QWRFGAGSYFAITVITIGYGHAAAPSTDDGKVF 108
Db 98 ELDELIIQIIVAINAGIIPLGNSSNQVSHWDLGSSFFFACTVITITIGFNGISPRTEGGKI 157
QY 109 FCMFYALLGIPLTVMFQSLGERINTLVRYLLHRAKKGGLGMRAD-----VSM 156
Db 158 FCIYVALLGIPLEGFLAGVDQLGTF-----GKIAKVEDTFIKWNVSTQKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAASHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQ 216
Db 209 ISTIIFILEGCVLFALPAVIFKHEGWSALDAIYFWITLTITIGFDYVAGSD--IEY 266
QY 217 QPOYVAFSFFVYILTLGLTVIGAFNLV--VLRFTMTNADEKRD-AEHRALLTRN 267
Db 267 LDFKPVVFWILVGLYFAAVLSMIGDWLRVSKTKKEVGEFRAHAEWTAN 320
```

```
RESULT 7
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match      18.1%; Score 369; DB 3; Length 411;
Best Local Similarity 31.6%; Pred. No. 7.1e-32;
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLRQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQPEISQRTTIVIQKTFIAQHACVNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITIGYGHAAAPSTDGKVK 108
DB 98 ELDELIQIIVAAINAGIIPLGNTSNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLGIPLTLMVQFQSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYALLGIPFLFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVITLTITIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILTGLTVIGAFNLV--VLRPMTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDMLRVISKTKKEEVGEFRAHAAEWATAN 320

; QUERY MATCH
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLRQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGATVFKALEQPEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITIGYGHAAAPSTDGKVK 108
DB 98 ELDELIQIIVAAINAGIIPLGNTSNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLGIPLTLMVQFQSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYALLGIPFLFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVITLTITIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILTGLTVIGAFNLV--VLRPMTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDMLRVISKTKKEEVGEFRAHAAEWATAN 320

; QUERY MATCH
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLRQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGATVFKALEQPEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITTTIGYGHAAAPSTDGKVK 108
```

```
DB 98 ELDELIQIIVAAINAGIIPLGNTSNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLGIPLTLMVQFQSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYALLGIPFLFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVITLTITIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILTGLTVIGAFNLV--VLRPMTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDMLRVISKTKKEEVGEFRAHAAEWATAN 320

RESULT 9
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PR1
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLRQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGATVFKALEQPEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRFAGSFYFAITVITTTIGYGHAAAPSTDGKVK 108
DB 98 ELDELIQIIVAAINAGIIPLGNTSNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLGIPLTLMVQFQSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYALLGIPFLFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVITLTITIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILTGLTVIGAFNLV--VLRPMTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDMLRVISKTKKEEVGEFRAHAAEWATAN 320

; QUERY MATCH
; TYPE: PR1
; ORGANISM: H. sapiens
US-09-336-643A-83
```

```
RESULT 10
US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
```







**This Page Blank (uspio)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:58:54 ; Search time 101.398 Seconds  
(without alignments)  
1567.669 Million cell updates/sec

Title: US-09-503-089A-4

Perfect score: 2090

Sequence: 1 MAAPDLLDPKSAQNSKPL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2090	100.0	411	3	Aae10342 Murine TR
2	2084	99.7	411	2	Aay28497 Mouse h-T
3	2044	97.8	411	2	Aay34133 Human pot
4	2044	97.8	411	2	Aay28496 h-TREK1 p
5	2044	97.8	411	4	Aab50044 Human TRE
6	2044	97.8	411	7	Adp03586 Human GPC
7	2044	97.8	411	8	Adq76698 Human two
8	2041	97.7	411	3	Aae10341 Human TRE
9	2038	97.5	422	7	Adp03575 Human GPC
10	2033	97.3	411	5	Aae16597 Human TWI
11	2011	96.2	426	4	Aau07618 Human pot
12	2007	96.0	426	4	Aau07622 Human pot
13	2006	96.0	426	4	Aau07623 Human pot
14	2003	95.8	426	4	Aau07625 Human pot
15	2002	95.8	426	4	Aau07624 Human pot
16	1864	89.2	370	2	Aay30648 A mechani
17	1820.5	77.5	337	6	ABR41487 Human DIT
18	1251.5	59.9	538	5	AAB47930 Human TRE
19	1251.5	59.9	538	5	Aae16596 Human TWI
20	1251.5	59.9	538	5	ABP69333 Human pot
21	1251.5	59.9	543	5	Aae21804 Human TRE
22	1251.5	59.9	543	5	Aau81354 Novel hum
23	1251.5	59.9	543	5	Aau79472 Human nov
24	1251.5	59.9	543	5	ABB83542 Hypothala
25	1251.5	59.9	543	6	ADA05746 Human NOV

26	1251.5	59.9	543	7	ADP08315	Ade08315 Novel pro
27	1251.5	59.9	543	8	ADN62910	Adn62910 Human NOV
28	1247.5	59.7	543	5	AAU79473	Aau79473 Human nov
29	1224	58.6	724	5	AAO14193	Aao14193 Human tra
30	951	45.5	228	8	ADJ27190	Adj27190 Human TRI
31	797	38.1	392	6	ABU60891	Abu60891 Human G p
32	797	38.1	393	3	AAy94426	Aay94426 Human h-T
33	797	38.1	393	3	AAy94425	Aay94425 Human h-T
34	797	38.1	393	4	AAG67777	Aag67777 Human mec
35	797	38.1	419	5	AAG78406	Aag78406 Amino aci
36	797	38.1	419	7	Aae38597	Aae38597 Human pot
37	797	38.1	419	7	ADK52550	Adk52550 Hematolog
38	797	38.1	419	8	ADH51639	Adh51639 Human 123
39	797	38.1	419	8	ADI27936	Adi27936 Human TWI
40	797	38.1	419	8	ADR44894	Adr44894 Polypept1
41	797	38.1	1314	4	AAU04571	Aau04571 Human G-p
42	797	38.1	1314	6	ABU60872	Abu60872 Human G p
43	770.5	36.9	398	2	AAy30647	Aay30647 A mechani
44	762.5	36.5	398	5	AAE16598	Aae16598 Human TWI
45	635.5	30.4	383	4	ABG02731	Abg02731 Novel hum

#### ALIGNMENTS

RESULT 1

AAE10342

ID AAE10342 standard; protein; 411 AA.

AC AAE10342;

DT 10-DEC-2001 (first entry)

DE Murine TREK-1 potassium channel protein.

KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia; amnesia.

OS Mus musculus.

PN WO200047738-A2.

PD 17-AUG-2000.

PF 11-FEB-2000; 2000WO-IB000226.

PR 12-FEB-1999; 99US-0119727P.

PR 11-FEB-2000; 2000US-00503089.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;

XX WPI; 2000-549146/50.

XX N-PSDB; AAD17497.

XX Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic properties.

XX Claim 9; Page 32-33; 39pp; English.

XX The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TREK-1 potassium channel protein

XX Sequence 411 AA;

SQ

Query Match 100.0%; Score 2090; DB 3; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-218; Indels 0; Gaps 0;  
 Matches 411; Conservative 0; Mismatches 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 61 GAAVFKALEQPOEISORTTIVIKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120

QY 121 SNOVSHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 DB 121 SNOVSHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAVIFKHIEGWSALD 240

QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAGELAGNHQ 360  
 DB 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAGELAGNHQ 360

QY 361 ELTPCRRTLTSVNHLTSEREVLPPLLKAESIYINGLTPHCAGEDIAVIENMK 411  
 DB 361 ELTPCRRTLTSVNHLTSEREVLPPLLKAESIYINGLTPHCAGEDIAVIENMK 411

RESULT 2  
 AAY28497  
 ID AAY28497 standard; protein; 411 AA.  
 AC AAY28497;  
 DT 12-OCT-1999 (first entry)  
 XX Mouse h-TREK1 polypeptide.  
 DE h-TREK1; two pore potassium channel; inflammatory disease;  
 KW Chromosome 1q32.  
 XX Mus musculus.  
 OS WO9937762-A1.  
 PN 29-JUL-1999.  
 PD 02-DEC-1998; 98WO-EF007805.  
 PF 27-JAN-1998; 98EP-00300570.  
 PR 09-OCT-1998; 98GB-00022135.  
 XX (SMK ) SMITHKLINE BEECHAM PLC.  
 PA Meadows HJ, Chapman CG;  
 XX WPI; 1999-469126/39.  
 PI N-PSDB; AA200040.  
 DR New two pore potassium channel used for, e.g. treatment of cancer,  
 CC pulmonary, cardiovascular and inflammatory diseases.  
 CC Claim 3; Page 26; 44pp; English.  
 XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
 CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel. The  
 CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or  
 CC susceptibility to a disease related to expression or activity of h-TREK-1

CC polypeptides. The methods of diagnosis may be used in the treatment of  
 CC diseases including cancer, pulmonary, cardiovascular, and inflammatory  
 CC diseases, pain, psychiatric disorders including depression and  
 CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
 CC and head trauma and neurological disorders including migraine  
 XX Sequence 411 AA;

Query Match 99.7%; Score 2084; DB 2; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-217; Indels 0; Gaps 0;  
 Matches 410; Conservative 0; Mismatches 1;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 61 GAAVFKALEQPOEISORTTIVIKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120

QY 121 SNOVSHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 DB 121 SNOVSHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAVIFKHIEGWSALD 240

QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAGELAGNHQ 360  
 DB 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAGELAGNHQ 360

QY 361 ELTPCRRTLTSVNHLTSEREVLPPLLKAESIYINGLTPHCAGEDIAVIENMK 411  
 DB 361 ELTPCRRTLTSVNHLTSEREVLPPLLKAESIYINGLTPHCAGEDIAVIENMK 411

RESULT 3  
 AAY34133  
 ID AAY34133 standard; protein; 411 AA.  
 XX AC AAY34133;  
 XX 30-NOV-1999 (first entry)  
 XX Human potassium channel K+Hnov59.  
 DE Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
 KW cardiovascular disorder; CNS disorder; renal disorder.  
 XX Homo sapiens.  
 XX WO9943696-A1.  
 XX 02-SEP-1999.  
 XX 22-FEB-1999; 99WO-US003826.  
 XX 25-FEB-1998; 98US-0076687P.  
 PR 07-AUG-1998; 98US-0095836P.  
 PR 19-JAN-1999; 99US-0116448P.  
 XX (AXYS-) AXYS PHARM INC.  
 XX Miller AP, Curran ME, Hu P, Rutter M, Wang J;  
 XX WPI; 1999-527591/44.  
 DR N-PSDB; AA211915.  
 XX

PT New nucleic acids encoding mammalian K-Hnov59 potassium channel proteins,  
 PT useful for the diagnosis and treatment of episodic ataxia with myokymia,  
 PT cardiac arrhythmia, epilepsy and Bartter's syndrome.

PS Claim 3; Page 104-105; 112pp; English.

XX This sequence represents the human K-Hnov59 potassium channel. K-Hnov  
 CC proteins have a high degree of homology to known potassium channels and  
 CC may be alpha subunits, which form the functional channel, or accessory  
 CC subunits that act to modulate the channel activity. K-Hnov59 is a 4  
 CC transmembrane domain, 2 pore domain potassium channel. The gene is  
 CC located on chromosome 19, determined via PCR chromosomal localisation  
 CC using primers AA211939 and AA211940. K-Hnov cDNAs were isolated by  
 CC extension of expressed sequence tags (ESTs) which were related but not  
 CC identical to known human potassium channels. Potential polymorphisms  
 CC detected as sequence variants between multiple independent clones.  
 CC Potassium channels have critical roles in various cell types and  
 CC biochemical pathways. Defective potassium channels are known to cause  
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia  
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium  
 CC channels are critical components of virtually all cells, it is likely  
 CC that abnormal potassium channels are also implicated in certain renal,  
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides  
 CC encoding K-Hnov proteins may be used for identifying homologous or  
 CC related proteins and the DNA sequences encoding them. They may be used to  
 CC produce compositions that modulate the expression and function of the  
 CC K-Hnov protein and in studying the biochemical pathways associated with  
 CC it. They may also be used for the recombinant production of K-Hnov  
 CC protein in fermentation cultures. Additionally, such nucleotides may be  
 CC used in gene therapy protocols for the treatment of diseases associated  
 CC with abnormal potassium channels

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 2; Length 411;

Best Local Similarity 96.4%; Pred. No. 3.5e-213;

Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSAINVMKKTSTVIFLWVLYLII 60

DB 1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVIFLWVLYLII 60

QY 61 GAAVFKALQPOEISQRTTIVIQKQTFIAQACVNSTELDELIQQIVAAINAGIPLGNS 120

DB 61 GATVFKALQPOEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIPLGNT 120

QY 121 SNQVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180

DB 121 SNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360

DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360

QY 361 ELTPCRRTLTSVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

DB 361 ELTPCRRTLTSERDVLPLPKTESIYINGLTPHCAGEEIAVIENIK 411

RESULT 4

AAV28496

ID AAY28496 standard; protein; 411 AA.

XX

AC AAY28496;

XX

DT 12-OCT-1999 (first entry)

XX h-TREK1 polypeptide.

XX h-TREK1; two pore potassium channel; inflammatory disease;

XX chromosome 1q32.

XX Homo sapiens.

XX WO9937762-A1.

XX 29-JUL-1999.

XX 02-DEC-1998; 98WO-EP007805.

XX 27-JAN-1998; 98EP-00300570.

XX 09-OCT-1998; 98GB-00022135.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Meadows HJ, Chapman CG;

XX WPI: 1999-469126/39.

XX N-PSDB; AA200039.

XX New two pore potassium channel used for, e.g. treatment of cancer,

XX pulmonary, cardiovascular and inflammatory diseases.

XX Claim 3; Page 24; 44pp; English.

XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1

XX polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and the

XX gene maps to human chromosome 1q32, between the markers DIS237 and

XX W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a

XX disease or susceptibility to a disease related to expression or activity

XX of h-TREK1 polypeptides. The methods of diagnosis may be used in the

XX treatment of diseases including cancer, pulmonary, cardiovascular, and

XX inflammatory diseases, pain, psychiatric disorders including depression

XX and schizophrenia, neurodegenerative diseases including Alzheimer's,

XX stroke, and head trauma and neurological disorders including migraine.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 2; Length 411;

Best Local Similarity 96.4%; Pred. No. 3.5e-213;

Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSAINVMKKTSTVIFLWVLYLII 60

DB 1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVIFLWVLYLII 60

QY 61 GAAVFKALQPOEISQRTTIVIQKQTFIAQACVNSTELDELIQQIVAAINAGIPLGNS 120

DB 61 GATVFKALQPOEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIPLGNT 120

QY 121 SNQVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180

DB 121 SNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360

DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360

QY 361 ELTPCRRTLTSVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

```

Db      361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEEIAVENIK 411
RESULT 5
ID      AAB50044 standard; protein; 411 AA.
XX
AC      AAB50044;
XX
DT      19-MAR-2001 (first entry)
XX
DE      Human TREK.
XX
KW      Human; TREK; 2p domain potassium channel; resting membrane potential;
KW      neuronal excitability; neurotransmitter release modulation; epilepsy;
KW      neurological disorder; sleep-related disorder; cognitive dysfunction;
KW      attention deficit disorder; addiction; anxiety; phobia;
KW      Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
KW      erectile dysfunction; alopecia.
XX
OS      Homo sapiens.
XX
PN      WO200072863-A2.
XX
PD      07-DEC-2000.
XX
PF      01-JUN-2000; 2000WO-CB002107.
XX
PR      01-JUN-1999; 99GB-00012733.
XX
PA      (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI      Hervieu GJ, Meadows HJ, Randall AD;
XX
WPI; 2001-080422/09.
DR      N-PSDB; AAC90412.
XX
Use of human TREK1 polypeptide, polynucleotides encoding them and
modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
disorders, addiction and dyskinesias including Parkinson's and
Huntington's chorea.
XX
Claim 7; Page 29; 35pp; English.
XX
The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the
2p domain potassium channel family of proteins which play a part in the
control of resting membrane potential. Modulation of these channels will
therefore affect neuronal excitability, thereby leading to a modulation
of neurotransmitter release and activity of neuronal networks. Such
modulation therefore may be useful for the treatment of certain
neurological conditions such as epilepsy, sleep-related disorders,
cognitive dysfunction, attention deficit disorder, addiction,
anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,
incontinence, erectile dysfunction or alopecia
XX
Sequence 411 AA;
Query Match          97.8%; Score 2044; DB 4; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-213;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY      1 MAAPDLLDPKSAQNSKPLSPSSKPTVLASVESDSAINVMKKTSTVFILVVLYLI 60
DB      1 MAAPDLLDPKSAQNSKPLSPSTPTVLASVESDSTINVMKKTSTVFILVVLYLI 60
QY      61 GAAVFKALPQPOEISORTTIVIKQOTFIAQACVNSTELDELIQIVAINAGIIPLGNS 120
DB      61 GATVFKALPQPEHISORTTIVIKQOTFISQHSVNSTELDELIQIVAINAGIIPLGNT 120
QY      121 SNQVSHWDLGSSFFAGTVTTTIGFNGISPRTEGGKIFCIIIVALLGIPFLGVLGVDQ 180
DB      121 SNQISHWDLGSSFFAGTVTTTIGFNGISPRTEGGKIFCIIIVALLGIPFLGVLGVDQ 180

```

---

```

QY      181 LGTIFGKGIKAVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVFKHIEGWSALD 240
DB      181 LGTIFGKGIKAVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVFKHIEGWSALD 240
QY      241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFYPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
DB      241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFYPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
QY      301 KKTKEEVGEPFAHAAEWNTAVTAFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360
DB      301 KKTKEEVGEPFAHAAEWNTAVTAFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360
QY      361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEEIAVENIK 411
DB      361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEEIAVENIK 411
RESULT 6
ID      ADP03586 standard; protein; 411 AA.
XX
AC      ADP03586;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Human GPCR potassium channel, subfamily K, member 2 protein.
XX
KW      GPCR; G-protein coupled receptor; neuroprotective; nootropic;
KW      tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
KW      anticonvulsant; antiparkinsonian; cytotostatic; cardiac; hypotensive;
KW      antianalgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;
KW      uropathic; antiulcer; antiallergic; cell cycle regulation; neurological;
KW      severe mental retardation; dyskinesia; brain; spinal cord; affective;
KW      neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
KW      eating; HIV infection; cancer; metabolic; pituitary;
KW      chromosome identification; gene therapy; human; receptor;
KW      potassium channel subfamily K member 2.
XX
OS      Homo sapiens.
XX
PN      WO20003062393-A2.
XX
PD      31-JUL-2003.
XX
PF      22-JAN-2003; 2003WO-US001911.
XX
PR      22-JAN-2002; 2002US-0350724P.
XX
PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI      Ramanathan CS, Gopal S, Mintier G, Feder JN;
XX
WPI; 2003-618283/58.
XX
New nucleic acid molecule encoding a human G-protein coupled receptor,
useful for diagnosing, preventing or treating diseases involving the
receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
cancer.
XX
Example 1; SEQ ID NO 31; 224pp; English.
XX
The invention relates to a novel isolated GPCR (G-protein coupled
receptor) nucleic acid molecule. The polynucleotide and polypeptide of
the invention demonstrate neuroprotective, nootropic, tranquiliser,
antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
antiparkinsonian, cytotostatic, cardiac, hypotensive, antianalgesic,
analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,
antiulcer and antiallergic properties. The nucleic acid molecule and
polypeptide of the invention may be useful in diagnosing, preventing,
treating or ameliorating a medical condition, such as a disorder related
to aberrant G-protein coupled signalling, a disorder related to aberrant
cell cycle regulation, neurological disorders, severe mental retardation
and dyskinesias, brain disorders, spinal cord disorders, affective

```

CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrinal diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor)  
 CC protein of the invention which was used for homology purposes.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 7; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSPSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPRLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIQKOTFIAQACVNSTELDELIQQIVAAINAGIIPLGNT 120  
 DB 61 GATVFKALEQPEISORTTIVIQKOTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120

QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180  
 DB 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300  
 DB 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360  
 DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

QY 361 ELTPCRRTLISVNHLSERDVLPLLKAEISYIYNGLTTPHCAGEDIAVIENMK 411  
 DB 361 ELTPCRRTLISVNHLSERDVLPLLKAEISYIYNGLTTPHCAGEDIAVIENIK 411

RESULT 7

ADQ76698  
 ID ADQ76698 standard; protein; 411 AA.

AC ADQ76698;

DT 07-OCT-2004 (first entry)

DE Human two pore domain potassium channel TREK-1.

XX TREK-1; sleep; two pore domain potassium channel; sedative; hypnotic;  
 KW human.

OS Homo sapiens.

XX WO2004058325-A2.

PN 15-JUL-2004.

XX 23-DEC-2003; 2003WO-US040913.

XX 23-DEC-2002; 2002US-0436201P.

XX (WISC ) WISCONSIN ALUMNI RES FOUND.

XX Tononi G, Cirelli C;

XX WPI; 2004-534024/51.

DR GENBANK; NM014217.

XX

PT Identifying a Drosophila mutant fly with a no rebound, short sleep and/or  
 no sleep deprivation resistant phenotype, for identifying sleep-related  
 molecular targets, comprises recording sleep quantity of the mutant fly.

PS Claim 12; SEQ ID NO 2; 83pp; English.

XX The present sequence is that of the human two pore domain K+ channel TREK  
 -1. In rats, TREK-1 is highly expressed in much of the brain and is  
 inhibited by protein kinase C and protein kinase C mediated  
 phosphorylation. It is activated by volatile general anaesthetics and is  
 expressed at high levels in the brain of sleep animals. Based on these  
 criteria and on experimental results, it is hypothesized that TREK-1 is a  
 key mediator of sleep (when open) and waking (when closed). The invention  
 provides methods for identifying a sleep- or wakefulness-promoting  
 compound based on the compound's ability to modulate the pore domain K+  
 channels such as TREK-1. It also provides screening methods for isolating  
 short sleep, no rebound and sleep deprivation resistant Drosophila  
 mutants useful for identifying sleep-related molecular targets.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 8; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSPSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQAQNSKPRLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIQKOTFIAQACVNSTELDELIQQIVAAINAGIIPLGNS 120

DB 61 GATVFKALEQPEISORTTIVIQKOTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120

QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

DB 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

QY 361 ELTPCRRTLISVNHLSERDVLPLLKAEISYIYNGLTTPHCAGEDIAVIENMK 411

DB 361 ELTPCRRTLISVNHLSERDVLPLLKAEISYIYNGLTTPHCAGEDIAVIENIK 411

RESULT 8

AAE10341

ID AAE10341 standard; protein; 411 AA.

XX AAE10341;

AC AAE10341;

DT 10-DEC-2001 (first entry)

DE Human TREK-1 potassium channel protein.

XX Human; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia.

XX Homo sapiens.

XX WO200047738-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-IB000226.  
 PF  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 XX  
 XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 FI  
 XX WPI; 2000-549146/50.  
 DR N-PSDB; AAD17496.  
 DR  
 XX  
 XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties.  
 XX  
 XX Claim 3; Page 28; 39pp; English.  
 PS  
 XX The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,  
 CC reversible state of unconsciousness with concurrent amnesia and analgesia  
 CC in a mammal upon inhalation. The present sequence is human TREK-1  
 CC potassium channel protein  
 CC  
 XX Sequence 411 AA;  
 SQ  
 Query Match 97.7%; Score 2041; DB 3; Length 411;  
 Best Local Similarity 96.1%; Pred. No. 7.5e-213;  
 Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTPTVLASRVESDTTINVMKWTSTFIPLVVLYLII 60  
 QY 61 GAAVFKALEQPOEISORTTIVIQKOTFFIAQACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 61 GATVFKALEQPOEISORTTIVIQKOTFFISQHCVCNSTELDELIQOIVAAINAGIPLGNT 120  
 QY 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIPFLGVLGAGVDQ 180  
 DB 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIPFLGVLGAGVDQ 180  
 QY 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
 QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWLVLGVLAYFAAIVLSMIGDWLRVIS 300  
 DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWLVLGVLAYFAAIVLSMIGDWLRVIS 300  
 QY 301 KKTKEEVGFRAHAETANVTAEKTEPRRLSVIYDKFORATSVKRLSAELAGNHQ 360  
 DB 301 KKTKEEVGFRAHAETANVTAEKTEPRRLSVIYDKFORATSVKRLSAELAGNHQ 360  
 QY 361 ELTPCRTLTVNHLTSERVLPLLKAESIYLNGLTTPHCAGRDIAVIENMK 411  
 DB 361 ELTPCRTLTVNHLINERDVLPLLKTESIYLNGLTTPHCAGEIAVIENIK 411

RESULT 9

ADP03575

ID ADP03575 standard; protein; 422 AA.

XX

AC ADP03575;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human GPCR twin pore channel" protein variant "Gene 9" protein.

XX

KW GPCR; G-protein coupled receptor; neuroprotective; nootropic;  
 KW tranquilizer; antimigraine; neuroleptic; antimanic; antidepressant;  
 KW anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive;  
 KW antianalgesic; anorectic; anti-HIV; antisthmatic; osteopathic;  
 KW antitumor; antitumor; antitumor; cell cycle regulation; neurological;  
 KW severe mental retardation; dyskinesia; brain; spinal cord; affective;  
 KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;  
 KW eating; HIV infection; cancer; metabolic; pituitary;  
 KW chromosome identification; gene therapy; human; receptor;  
 KW twin pore channel; potassium channel subfamily K member 2 variant.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2003062393-A2.  
 XX  
 XX 31-JUL-2003.  
 XX  
 XX 22-JAN-2003; 2003WO-US001911.  
 XX  
 XX 22-JAN-2002; 2002US-0350724P.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Ramanathan CS, Gopal S, Mintier G, Feder JN;  
 PI  
 XX WPI; 2003-618283/58.  
 DR N-PSDB; ADP03564.  
 DR  
 XX New nucleic acid molecule encoding a human G-protein coupled receptor,  
 PT useful for diagnosing, preventing or treating diseases involving the  
 PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or  
 PT cancer.  
 XX  
 PS Claim 5; SEQ ID NO 20; 224pp; English.

XX The invention relates to a novel isolated GPCR (G-protein coupled  
 CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
 CC the invention demonstrate neuroprotective, nootropic, tranquilizer,  
 CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,  
 CC antiparkinsonian, cytostatic, cardiant, hypotensive, antianalgesic,  
 CC analgesic, anorectic, anti-HIV, antisthmatic, osteopathic, uropathic,  
 CC antitumor and antitumor properties. The nucleic acid molecule and  
 CC polypeptide of the invention may be useful in diagnosing, preventing,  
 CC treating or ameliorating a medical condition, such as a disorder related  
 CC to aberrant G-protein coupled signaling, a disorder related to aberrant  
 CC cell cycle regulation, neurological disorders, severe mental retardation  
 CC and dyskinesias, brain disorders, spinal cord disorders, affective  
 CC disorders, neoplastic disorders, cardiovascular disorders, growth  
 CC disorders, immune-related disorders, endocrinal diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor)  
 CC protein which was isolated by the method of the invention.  
 XX  
 SQ Sequence 422 AA;

Query Match 97.5%; Score 2038; DB 7; Length 422;

Best Local Similarity 95.9%; Pred. No. 1.7e-212;

Matches 394; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVLYLII 60  
 DB 12 LAAPDLLDPKSAQAQNSKPRLSFSTPTVLASRVESDTTINVMKWTSTFIPLVVLYLII 71  
 QY 61 GAAVFKALEQPOEISORTTIVIQKOTFFIAQACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 72 GATVFKALEQPOEISORTTIVIQKOTFFISQHCVCNSTELDELIQOIVAAINAGIPLGNT 131  
 QY 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIPFLGVLGAGVDQ 180  
 DB 132 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIPFLGVLGAGVDQ 191

QY 181 LGTIFGKGIKAVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 |||||  
 DB 192 LGTIFGKGIKAVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 251  
 |||||  
 QY 241 AIYFVVITLTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 DB 252 AIYFVVITLTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 311  
 |||||  
 QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLKSLAELAGNHQ 360  
 |||||  
 DB 312 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLKSLAELAGNHQ 371  
 |||||  
 QY 361 ELTPCRRTLSVNLHLSERVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411  
 |||||  
 DB 372 ELTPCRRTLSVNLHLSERDVLPPLLKTESIYLNGLTPHCAGEDIAVIENIK 422  
 |||||

## RESULT 10

AAE16597  
 ID AAE16597 standard; protein; 411 AA.

XX AC AAE16597;

DT 18-APR-2002 (first entry)

XX Human TWIK-Related K+ Channel-1 (TREK-1) protein.

DE Human TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

KW Human; TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 47..65  
 FT /note= "M1 membrane spanning segment"  
 FT Domain 127..150  
 FT /note= "P1 pore domain"  
 FT Region 158..178  
 FT /note= "M2 membrane spanning segment"  
 FT Region 209..230  
 FT /note= "M3 membrane spanning segment"  
 FT Domain 236..259  
 FT /note= "P2 pore domain"  
 FT Region 274..293  
 FT /note= "M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-1B001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX New mammalian K+ channel protein with two pore domains, for screening  
 PT various compounds, particularly for identifying biologically active  
 PT compounds with anaesthetic properties.

XX Disclosure; Fig 1A; 50pp; English.

XX The invention relates to a mammalian K+ channel protein with two pore  
 CC domains, called TREK2 (TWIK-Related K+ Channel). The protein produces  
 CC currents whose current-voltage relationship is slightly inwardly  
 CC rectifying in high symmetrical K+ conditions. TREK2 is a member of the  
 CC fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene  
 CC located on chromosome 14q31 is abundantly expressed in kidney, pancreas

CC and moderately in testis, brain, colon and small intestine. The mammalian  
 CC K+ channel protein is useful in methods for screening various compounds.  
 CC In particular, the protein is useful in methods for identifying  
 CC biologically active compounds with anaesthetic properties. The present  
 CC sequence is TREK-1 protein used in the invention

XX Sequence 411 AA;

Query Match 97.3%; Score 2033; DB 5; Length 411;  
 Best Local Similarity 95.9%; Pred. No. 5.6e-212;  
 Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSPSSKPTVLASRVESDAINVMKWKTVSTIFLVVLII 60  
 |||||  
 DB 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTINVMKWKTVSTIFLVVLII 60  
 |||||  
 QY 61 GAAVFKALEQPOEISORTTIVIQKOTFIAQHACVNSTELDELIIQIIVAAINAGIIPLGNT 120  
 |||||  
 DB 61 GATVFKALEQPEIISORTTIVIQKQTFIISQVNSTELDELIIQIIVAAINAGIIPLGNT 120  
 |||||  
 QY 121 SNQVSHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180  
 |||||  
 DB 121 SNQISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180  
 |||||  
 QY 181 LGTIFGKGIKAVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 |||||  
 DB 181 LGTIFGKGIKAVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 |||||  
 QY 241 AIYFVVITLTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 DB 241 AIYFVVITLTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLKSLAELAGNHQ 360  
 |||||  
 DB 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLKSLAELAGNHQ 360  
 |||||  
 QY 361 ELTPCRRTLSVNLHLSERVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411  
 |||||  
 DB 361 ELTPCRRTLSVNLHLSERDVLPPLLKTESIYLNGLTPHCAGEDIAVIENIK 411  
 |||||

## RESULT 11

AAU07618  
 ID AAU07618 standard; protein; 426 AA.

XX AC AAU07618;

XX 21-NOV-2001 (first entry)

XX Human potassium ion channel TPKC1 protein.

XX Transmembrane potassium ion channel protein; inward potassium flux;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human.

XX Homo sapiens.

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI ) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12169.

XX New polypeptide, a mutant potassium ion channel protein for improving







```

XX DE Human potassium ion channel TPKC1 mutant protein #2.
XX
XX Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human; mutant; muten.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 272 /note= "Wild-type Tyr replaced by His"
FT
XX
XX WO200161006-A2.
XX
XX 23-AUG-2001.
XX
XX 14-FEB-2001; 2001WO-US004680.
XX
XX 15-FEB-2000; 2000US-00503849.
XX
XX (BADI ) BASF CORP.
XX
XX Pausch MH;
XX
XX WPI; 2001-536570/59.
XX
XX N-PSDB; AAS12182.
XX
XX New polypeptide, a mutant potassium ion channel protein for improving
XX inward potassium flux under acidic conditions.
XX
XX Claim 37; Page 115-117; 131pp; English.
XX
XX The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a human transmembrane potassium ion channel TPKC1 mutant
XX protein
XX
XX Sequence 426 AA;
XX
XX Query Match 96.0%; Score 2006; DB 4; Length 426;
XX Best Local Similarity 94.9%; Pred. No. 5.2e-209;
XX Matches 390; Conservative 14; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTINVMKWTSTIFLVVLYLII 75
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 61 GAAVFKALEQPOEISORTTIVIOKQTFIAQHCNVNSTELDELIIQIVAAINAGIIPLGNS 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 76 GATVFKALEQPHISORTTIVIOKQTFISQHCNVNSTELDELIIQIVAAINAGIIPLGNT 135
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 121 SNOVSHWDLGSSFFAGTVITTTGFGNISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 180
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 136 SNOIISHWDLGSSFFAGTVITTTGFGNISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 195
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 181 LGTIFGKGIKAVEDTFIKWNSQTKRIITSTIIFILPGCVLFVALPAVIFKHEGHSALD 240
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 196 LGTIFGKGIKAVEDTFIKWNSQTKRIITSTIIFILPGCVLFVALPAIIPKHEGHSALD 255
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 241 AIYFVWITLTIGFGDVVAGGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 256 AIYFVWITLTIGFGDVVAGGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDLVRVIS 315
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 301 KKTKEEVEGFEPAHAAEWNTANVTAEFKETRRRLSVEIYDKFQRATSKRKLASLGNHQQ 360
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX Db 316 KKTKEEVEGFEPAHAAEWNTANVTAEFKETRRRLSVEIYDKFQRATSKRKLASLGNHQQ 375
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 361 ELTPCRRTLNVNHLTSEREVLPPLKAESIYLNGLTPHCAGEDIAVIENMK 411
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX Db 376 ELTPCRRTLNVNHLTSERDVLPPLKTESIYLNGLAPHACGABEIAVIENIK 426
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX RESULT 14
XX AAU07625
XX ID AAU07625 standard; protein; 426 AA.
XX
XX AC AAU07625;
XX
XX XX 21-NOV-2001 (first entry)
XX
XX DE Human potassium ion channel TPKC1 mutant protein #4.
XX
XX KW Transmembrane potassium ion channel protein; inward potassium flux;
XX pest control; membrane potential; pesticide; antihelminthic; nematode;
XX insect; TPKC1; human; mutant; muten.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 270 /note= "Wild-type Gly replaced by Arg"
XX
XX PN WO200161006-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 14-FEB-2001; 2001WO-US004680.
XX
XX PR 15-FEB-2000; 2000US-00503849.
XX
XX PA (BADI ) BASF CORP.
XX
XX PI Pausch MH;
XX
XX DR WPI; 2001-536570/59.
XX
XX DR N-PSDB; AAS12184.
XX
XX PT New polypeptide, a mutant potassium ion channel protein for improving
XX inward potassium flux under acidic conditions.
XX
XX PS Claim 37; Page 119-120; 131pp; English.
XX
XX CC The invention relates to a mutant potassium ion channel protein, having
XX four membrane spanning domains and two pore forming domains, comprising a
XX mutation at the second pore forming domain. The expression of the mutant
XX protein in a cell confers improved inward potassium flux and the ability
XX to grow in the presence of potassium. Mutant proteins and their
XX corresponding polynucleotide sequences can therefore be used to improve
XX inward potassium flux into cells under acidic conditions by modulating
XX the membrane potential using therapeutic agents. The sequences may be
XX used to develop agonists and antagonists of potassium channel proteins in
XX order to control pests such as nematodes and insects. This sequence
XX represents a human transmembrane potassium ion channel TPKC1 mutant
XX protein
XX
XX SQ Sequence 426 AA;
XX
XX Query Match 95.8%; Score 2003; DB 4; Length 426;
XX Best Local Similarity 94.9%; Pred. No. 1.1e-208;
XX Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTINVMKWTSTIFLVVLYLII 75
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 61 GAAVFKALEQPOEISORTTIVIOKQTFIAQHCNVNSTELDELIIQIVAAINAGIIPLGNS 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX SQ Sequence 426 AA;
XX
XX Query Match 95.8%; Score 2003; DB 4; Length 426;
XX Best Local Similarity 94.9%; Pred. No. 1.1e-208;
XX Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTINVMKWTSTIFLVVLYLII 75
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 61 GAAVFKALEQPOEISORTTIVIOKQTFIAQHCNVNSTELDELIIQIVAAINAGIIPLGNS 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX

```

Db 76 GATVEKALEQPHETISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 135  
Qy 121 SNOVSHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIYVALLGIFLFGFLLAGVGDQ 180  
Db 136 SNOVSHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIYVALLGIFLFGFLLAGVGDQ 195  
Qy 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
Db 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 255  
Qy 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAFLSMIGDLWRVIS 300  
Db 256 AIYFVVTITLTIGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAFLSMIGDLWRVIS 315  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAETKTRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360  
Db 316 KKTKEEVGEFRAHAAEWNTAVTAETKTRRLRSVEIYDKFORATSVKRLSAELAGNHQ 375  
Qy 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411  
Db 376 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 426

RESULT 15  
AAU07624

ID AAU07624 standard; protein; 426 AA.

XX AAU07624;

XX 21-NOV-2001 (first entry)

XX Human potassium ion channel TPKC1 mutant protein #3.

XX Transmembrane potassium ion channel protein; inward potassium flux;

XX pest control; membrane potential; pesticide; antihelminthic; nematode;

XX insect; TPKC1; human; mutant; muten.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 272

FT /note= "Wild-type Tyr replaced by His"

FT Misc-difference 274

FT /note= "Wild-type Ala replace by Val"

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI ) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12183.

XX New polypeptide, a mutant potassium ion channel protein for improving

XX inward potassium flux under acidic conditions.

XX Claim 37; Page 117-119; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
XX four membrane spanning domains and two pore forming domains, comprising a  
XX mutation at the second pore forming domain. The expression of the mutant  
XX protein in a cell confers improved inward potassium flux and the ability  
XX to grow in the presence of potassium. Mutant proteins and their  
XX corresponding polynucleotide sequences can therefore be used to improve  
XX inward potassium flux into cells under acidic conditions by modulating  
XX the membrane potential using therapeutic agents. The sequences may be

CC used to develop agonists and antagonists of potassium channel proteins in  
CC order to control pests such as nematodes and insects. This sequence  
CC represents a human transmembrane potassium ion channel TPKC1 mutant  
CC protein

XX Sequence 426 AA;

Query Match 95.8%; Score 2002; DB 4; Length 426;

Best Local Similarity 94.6%; Pred. No. 1.4e-208;

Matches 389; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQAQNSKPRLSFSKPTVLAASRVSDSAINVMKMTVSTIFLVVLYLII 60

Db 16 VAAPDLLDPKSAQAQNSKPRLSFSKPTVLAASRVSDTTINVMKMTVSTIFLVVLYLII 75

Qy 61 GAAPFKALEQPHETISQRTTIVIQKTFIAQACNVSTELDELIQQIVAAINAGIPLGNS 120

Db 76 GATVFKALEQPHETISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 135

Qy 121 SNOVSHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIYVALLGIFLFGFLLAGVGDQ 180

Db 136 SNOVSHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIYVALLGIFLFGFLLAGVGDQ 195

Qy 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Db 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 255

Qy 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAFLSMIGDLWRVIS 300

Db 256 AIYFVVTITLTIGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAFLSMIGDLWRVIS 315

Qy 301 KKTKEEVGEFRAHAAEWNTAVTAETKTRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360

Db 316 KKTKEEVGEFRAHAAEWNTAVTAETKTRRLRSVEIYDKFORATSVKRLSAELAGNHQ 375

Qy 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

Db 376 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 426

Search completed: July 13, 2005, 08:39:47

Job time : 102.398 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 93.9622 Seconds  
(without alignments)  
2239.886 Million cell updates/sec

Title: US-09-503-089A-4  
Perfect score: 2090  
Sequence: 1 MAAPDLLDPKSAQNSKPKL.....LNGLTPHCAGEDIAVNIENMK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	100.0	411	1 CIW2 MOUSE	P97438 mus musculu
2	2082	99.6	414	2 O6P6P9	O6P6P9 mus musculu
3	2061	98.6	426	2 Q920B6	Q920B6 rattus norv
4	2044	97.8	411	2 Q9NRT2	Q9NRT2 homo sapien
5	2034	97.3	411	2 O8HY88	O8HY88 bos taurus
6	2011	96.2	426	1 CIW2 HUMAN	O95069 homo sapien
7	1261.5	60.4	538	2 O6Q834	O6Q834 oryctolagus
8	1256.5	60.1	453	2 O8B2B0	O8B2B0 m mus muscu
9	1256.5	60.1	535	2 O8BUW1	O8BUW1 m mus muscu
10	1256.5	60.1	538	1 CIWA RAT	Q91184 rattus norv
11	1251.5	59.9	538	1 CIWA HUMAN	P57789 homo sapien
12	1251.5	59.9	543	2 O6B0I4	O6B0I4 homo sapien
13	1223.5	58.5	546	2 O68EY1	O68EY1 xenopus lae
14	797	38.1	393	1 CIW4 HUMAN	O84454 mus musculu
15	770.5	36.9	398	1 CIW4 MOUSE	O84454 mus musculu
16	757.5	36.2	397	2 Q924I4	Q924I4 rattus norv
17	624	29.9	241	2 O9CX88	O9CX88 m mus muscu
18	499.5	23.9	309	1 CIW6 HUMAN	Q96T55 homo sapien
19	493.5	23.6	294	2 O6X6Z5	O6X6Z5 homo sapien
20	482.5	23.1	152	2 O6ZW95	O6ZW95 homo sapien
21	453	21.7	262	2 O6X6Z3	O6X6Z3 homo sapien
22	447	21.4	322	2 O6X6Z4	O6X6Z4 homo sapien
23	434.5	20.8	448	2 O6PFU3	O6PFU3 brachydanio
24	420	20.1	499	1 CIW5 HUMAN	O95279 homo sapien
25	409	19.6	502	2 O9JK62	O9JK62 m potassium
26	404	19.3	341	2 O8HZT2	O8HZT2 bos taurus
27	403.5	19.3	257	2 O80XE0	O80XE0 mus musculu
28	402.5	19.3	307	2 O80IT4	O80IT4 xenopus lae
29	395	18.9	184	2 O8N4V5	O8N4V5 homo sapien
30	389	18.6	332	1 CIW4 HUMAN	O96T54 homo sapien
31	377	18.0	336	2 O8R454	O8R454 cavia porce

32	377	18.0	336	2	Q99L99	Q99L99 mus musculu
33	376.5	18.0	336	1	CIW1 HUMAN	O00180 homo sapien
34	375.5	18.0	336	2	Q922T2	Q922T2 rattus norv
35	370	17.7	336	1	CIW1 MOUSE	O08581 mus musculu
36	370	17.7	394	1	CIW3 HUMAN	O14649 homo sapien
37	364.5	17.4	331	2	O8AVI5	O8AVI5 xenopus lae
38	353.5	16.9	259	2	O02821	O02821 oryctolagus
39	351.5	16.8	330	1	CIW6 HUMAN	Q9H427 homo sapien
40	351.5	16.8	365	1	CIW9 CAVPO	Q9J158 cavia porce
41	351	16.8	323	2	Q6PEI1	Q6PEI1 brachydanio
42	351	16.8	409	1	CIW3 MOUSE	O35111 mus musculu
43	351	16.8	411	1	CIW3 RAT	O54912 rattus norv
44	346.5	16.6	374	2	O632I0	O632I0 xenopus lae
45	345.5	16.5	396	2	Q923V6	Q923V6 rattus norv

#### ALIGNMENTS

#### RESULT 1

CIW2\_MOUSE  
ID CIW2\_MOUSE STANDARD; PRT; 411 AA.

AC P97438;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+ channel subunit).  
GN Name=Kcnk2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=97157476; PubMed=9003761;  
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;  
RT "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel.";  
RL EMBO J. 15:6854-6862(1996).  
[2]  
RP REVISIONS.  
RC TISSUE=Brain;  
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;  
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
RP ACTIVATION.  
RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;  
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";  
RL Nat. Neurosci. 2:422-426(1999).  
CC -!- FUNCTION: Outward rectifying potassium channel.  
CC -!- SUBUNIT: Homodimer (Potential).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: High expression in brain and lung. Also detected in kidney, heart and skeletal muscle. Not detected in liver. In the brain, highest expression in olfactory bulb, hippocampus and cerebellum.  
CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general anaesthetics such as chloroform, diethyl ether, halothane and isoflurane.  
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DE EMBL; U73488; AAC53005.2; -;  
DR MGD; MGI:109366; Kcnk2.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.  
DR GO; GO:0006813; P:potassium ion transport; IDA.  
DR InterPro; IPR003280; K+channel 2pore.  
DR InterPro; IPR001622; K+channel pore.  
DR InterPro; IPR003976; P:potassium ion transport; IDA.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
DR Glycoprotein; Ion transport; Ionic channel; Potassium;  
KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
FT DOMAIN 1 46 Cytoplasmic (Potential).  
FT TRANSMEM 47 67 Potential.  
FT DOMAIN 129 155 Pore-forming 1 (Potential).  
FT TRANSMEM 157 177 Potential.  
FT DOMAIN 178 207 Cytoplasmic (Potential).  
FT TRANSMEM 208 228 Potential.  
FT DOMAIN 238 268 Pore-forming 2 (Potential).  
FT TRANSMEM 273 293 Potential.  
FT DOMAIN 294 411 Cytoplasmic (Potential).  
FT DOMAIN 378 411 Essential for chloroform and haloethane  
FT sensitivity.  
FT 354 411 Required for basal channel activity.  
FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 119 119 N-linked (GlcNAc. .) (Potential).  
SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;

Query Match 100.0%; Score 2090; DB 1; Length 411;  
Best Local Similarity 100.0%; Pred. No. 4.3e-133;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKMTVSTIFLVVLYLII 60  
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKMTVSTIFLVVLYLII 60  
  
QY 61 GAAVFKALEQPEQISQRTTIVIQKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120  
DB 61 GAAVFKALEQPEQISQRTTIVIQKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120  
  
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIYALLGIFLFGVLLAGVGQ 180  
DB 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIYALLGIFLFGVLLAGVGQ 180  
  
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240  
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240  
  
QY 241 AIYFVVITLTITGFDYVAGSDIEYDFKPVVFWFVLVGLAYFAAVLSMTGDLWRVIS 300  
DB 241 AIYFVVITLTITGFDYVAGSDIEYDFKPVVFWFVLVGLAYFAAVLSMTGDLWRVIS 300  
  
QY 301 KKTKEVGFRAHAETANTVAETKTRRLSVIYDFKFORATSVKRLSIAELAGNHQ 360  
DB 301 KKTKEVGFRAHAETANTVAETKTRRLSVIYDFKFORATSVKRLSIAELAGNHQ 360  
  
QY 361 ELTPCRRILSVNHLISERVLPLKAEISYINGLTPHCAGEDIAVIENMK 411  
DB 361 ELTPCRRILSVNHLISERVLPLKAEISYINGLTPHCAGEDIAVIENMK 411

RESULT 2

Q6P6P9

ID Q6P6P9 PRELIMINARY; PRT; 414 AA.

AC Q6P6P9;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Kcnk2 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
CC (TC 1.A.1.8) family.  
CC EMBL; BC062094; AAHG2094.1; -;  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.  
DR GO; GO:0006813; P:potassium ion transport; IDA.  
DR GO; GO:0030322; P:stabilization of membrane potential; TAS.  
DR InterPro; IPR003280; K+channel 2pore.  
DR InterPro; IPR001622; K+channel pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
KW Ion transport; Ionic channel; Transmembrane; Transport.  
SQ SEQUENCE 414 AA; 45555 MW; 27F52D51DF6C66F8 CRC64;  
  
Query Match 99.6%; Score 2082; DB 2; Length 414;  
Best Local Similarity 99.5%; Pred. No. 1.5e-132;  
Matches 409; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKMTVSTIFLVVLYLII 60  
DB 4 VAAPELLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKMTVSTIFLVVLYLII 63  
  
QY 61 GAAVFKALEQPEQISQRTTIVIQKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120  
DB 64 GATVFKALEQPEQISQRTTIVIQKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 123  
  
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIYALLGIFLFGVLLAGVGQ 180  
DB 124 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIYALLGIFLFGVLLAGVGQ 183  
  
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240  
DB 184 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 243  
  
QY 241 AIYFVVITLTITGFDYVAGSDIEYDFKPVVFWFVLVGLAYFAAVLSMTGDLWRVIS 300  
DB 241 AIYFVVITLTITGFDYVAGSDIEYDFKPVVFWFVLVGLAYFAAVLSMTGDLWRVIS 300

Db 244 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 303  
 QY 301 KKTKEEVGEFRAHAAEWTANVTAEPKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360  
 Db 304 KKTKEEVGEFRAHAAEWTANVTAEPKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 363  
 QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411  
 Db 364 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 414

RESULT 3  
 Q2086 PRELIMINARY; PRT; 426 AA.

AC Q92086  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE 2P domain potassium channel KCNK2 (Tandem pore domain potassium channel TREK-1) (Arachidonic acid sensitive tandem pore domain potassium channel).  
 DE Name=Kcnk2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21219399; PubMed=11319556;  
 RA Bockenhauer D., Zilberberg N., Goldstein S.A.;  
 RT "KCNK2: reversible conversion of a hippocampal potassium leak into a  
 RT voltage-dependent channel.";  
 RL Nat. Neurosci. 4:486-491(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RX MEDLINE=21896087; PubMed=11897838;  
 RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,  
 RA Karschin A., Derst C., Steinlein O.K., Daut J.;  
 RT "Expression pattern and functional characteristics of two novel splice  
 RT variants of the two-pore-domain potassium channel TREK-2.";  
 RL J. Physiol. 539:657-668(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RA Li Z.B., Wang X.L.;  
 RT "Possible role of TREK-1 in temperature regulation.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 DR EMBL; AF325671; AAL01159.1; -;  
 DR EMBL; AF385402; AAL95708.1; -;  
 DR EMBL; AY695826; AAU06141.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR PRINTS; PR01333; 2PORECHANNEL.  
 DR PRINTS; PR01499; TREKCHANNEL.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 426 AA; 46912 MW; CACDA05BBE95FDBC CRC64;

Query Match 98.6%; Score 2061; DB 2; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 4.1e-131; Indels 0; Gaps 0;  
 Matches 404; Conservative 3; Mismatches 4;

QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKKTSTFVLVYLII 60  
 Db 16 VAAPDLDPKSAQNSKPRLSFSAKPTVLASRVESDSAINVMKKTSTFVLVYLII 75  
 QY 61 GAAVFKALPOEISORTTIVIKQNFIAQHACVNSTELDELIQIVTAINAIPLGNN 120

Db 76 GATVFKALPOEISORTTIVIKQNFIAQHACVNSTELDELIQIVTAINAIPLGNN 135  
 QY 121 SNQSHWDLGSSFFAGTVITITGFGNISPRTEGGKIPICIIYALLGIPLFGFLLAGVGQD 180  
 Db 136 SNQSHWDLGSSFFAGTVITITGFGNISPRTEGGKIPICIIYALLGIPLFGFLLAGVGQD 195  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLVALPAVFKHIEGHSALD 240  
 Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLVALPAVFKHIEGHSALD 255  
 QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
 Db 256 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 315  
 QY 301 KKTKEEVGEFRAHAAEWTANVTAEPKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 360  
 Db 316 KKTKEEVGEFRAHAAEWTANVTAEPKTRRRRLSVIYDKFORATSVKRLKSLAELAGNHQ 375  
 QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411  
 Db 376 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 426

RESULT 4  
 Q9NR12 PRELIMINARY; PRT; 411 AA.

AC Q9NR12  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily  
 DE K, member 2).  
 GN Name=TREK-1; Synonyms=KCNK2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20244931; PubMed=10784345;  
 RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,  
 RA Medhurst A.D., Murdock P., Chapman C.G.;  
 RT "Cloning, localisation and functional expression of the human  
 RT orthologue of the TREK-1 potassium channel.";  
 RL Pflugers Arch. 439:714-722(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;

RA Strausberg R.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 DR EMBL; AF171068; AAF89743.1; -;  
 DR EMBL; BC069462; AAF69462.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005216; F: ion channel activity; IEA.  
 DR GO; GO:0005267; P: potassium channel activity; IEA.  
 DR GO; GO:0006811; P: ion transport; IEA.  
 DR GO; GO:0006813; P: potassium ion transport; IEA.  
 DR GO; GO:0006813; P: potassium ion transport; IEA.  
 DR InterPro; IPR003280; K-channel\_2pore.  
 DR InterPro; IPR001622; K-channel\_pore.  
 DR InterPro; IPR003976; Trek channel.  
 DR PRINTS; PR01333; 2PORECHANNEL.  
 DR PRINTS; PR01499; TREKCHANNEL.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 97.8%; Score 2044; DB 2; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 5 5e-130;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60  
 QY 61 GAAVFKALPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 61 GATVFKALQEPHEISQRTTIVIQKQTFISQHCVNSTELDELIQOIVAAINAGIPLGNT 120  
 QY 121 SNQVSHWDLGSSFFPAGTVITITIGFNIISPRTEGGKIFCIYIALLGIPFLGFLAGVGDQ 180  
 DB 121 SNQVSHWDLGSSFFPAGTVITITIGFNIISPRTEGGKIFCIYIALLGIPFLGFLAGVGDQ 180  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDMLRVIS 300  
 DB 241 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDMLRVIS 300  
 QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
 QY 361 ELTPCRRTLTVNHLTSEREVLPPLLKAEISYINGLTPHCAGEDIAVIENMK 411  
 DB 361 ELTPCRRTLTVNHLTSEREVLPPLLKAEISYINGLTPHCAGEDIAVIENMK 411

RESULT 5  
 Q8HY88 PRELIMINARY; PRT; 411 AA.  
 AC Q8HY88;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Potassium channel subfamily K member 2.  
 GN Name=Kcnk2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=adrenal cortex;  
 RX MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;  
 RA Enyeart J.J., Xu L., Danti S., Enyeart J.A.;  
 RT "An ACTH- and ATP-regulated background K+ channel in adrenocortical  
 cells is TREK-1.";

RL J. Biol. Chem. 277:49186-49199(2002).  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 DR EMBL; AY148474; AAN37591.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005216; F: ion channel activity; IEA.  
 DR GO; GO:0005267; P: potassium channel activity; IEA.  
 DR GO; GO:0006811; P: ion transport; IEA.  
 DR GO; GO:0006813; P: potassium ion transport; IEA.  
 DR InterPro; IPR003280; K-channel\_2pore.  
 DR InterPro; IPR001622; K-channel\_pore.  
 DR InterPro; IPR003976; Trek channel.  
 DR PRINTS; PR01333; 2PORECHANNEL.  
 DR PRINTS; PR01499; TREKCHANNEL.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;

Query Match 97.3%; Score 2034; DB 2; Length 411;  
 Best Local Similarity 96.1%; Pred. No. 2.6e-129;  
 Matches 395; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60  
 DB 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLASRVSDTTINVMKWTSTIFLVVLYLII 60  
 QY 61 GAAVFKALPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
 DB 61 GATVFKALQEPHEISQRTTIVIQKQTFISQHCVNSTELDELIQOIVAAINAGIPLGNT 120  
 QY 121 SNQVSHWDLGSSFFPAGTVITITIGFNIISPRTEGGKIFCIYIALLGIPFLGFLAGVGDQ 180  
 DB 121 SNQVSHWDLGSSFFPAGTVITITIGFNIISPRTEGGKIFCIYIALLGIPFLGFLAGVGDQ 180  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240  
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDMLRVIS 300  
 DB 241 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDMLRVIS 300  
 QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
 QY 361 ELTPCRRTLTVNHLTSEREVLPPLLKAEISYINGLTPHCAGEDIAVIENMK 411  
 DB 361 ELTPCRRTLTVNHLTSEREVLPPLLKAEISYINGLTPHCAGEDIAVIENIK 411

RESULT 6  
 CIW2\_HUMAN STANDARD; PRT; 426 AA.  
 ID CIW2\_HUMAN  
 AC O95069; Q9UNE3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium  
 channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore  
 potassium channel TPCK1).  
 GN Name=KCNK2; Synonyms=TREK, TREK1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K+  
 channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 RN [2]











CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

ENBL; AF196965; AAF75132.1; -;	
DR InterPro; IPR003280; K-channel_2pore.	
DR InterPro; IPR001622; K-channel_pore.	
DR InterPro; IPR003976; Irek channel.	
DR PRINTS; PR01333; 2PORECHANNEL.	
DR PRINTS; PR01499; TREKCHANNEL.	
KW Glycoprotein; Ion transport; Ionic channel; Potassium;	
KW Potassium channel; Transmembrane; Voltage-gated channel.	
FT DOMAIN 1	Potential.
FT FT 71	Cytoplasmic (Potential).
FT TRANSMEM 72	Potential.
FT DOMAIN 154	Pore-forming 1 (Potential).
FT TRANSMEM 182	Potential.
FT DOMAIN 203	Cytoplasmic (Potential).
FT TRANSMEM 234	Potential.
FT TRANSMEM 254	Pore-forming 2 (Potential).
FT DOMAIN 263	Potential.
FT TRANSMEM 299	Cytoplasmic (Potential).
FT DOMAIN 320	N-linked (GlcNAC. .) (potential).
FT CARBOHYD 144	N-linked (GlcNAC. .) (potential).
FT CARBOHYD 147	1PF3F0AA52B97E4 CRC64;
SO SEQUENCE 538 AA; 59800 MW;	

SEQUENCE FROM N.A. (ISOFORM A).  
MEDLINE=204357899; PubMed=1080510; DOI=10.1074/jbc.M002822200;  
Lesage F., Terrenoire C., Rameau G., Lazdunski M.;  
"Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple  
regulations by polyunsaturated fatty acids, lysophospholipids and Gs,  
Gi, and Gq protein-coupled receptors.";  
J. Biol. Chem. 275:28398-28405(2000).  
[2]  
SEQUENCE FROM N.A. (ISOFORMS B AND C).  
MEDLINE=21896087; PubMed=11897838;  
Gu W., Schlichter G., Hirsch J.R., Engels H., Karachin C.,  
Karachin A., Derst C., Steinlein O.K., Daut J.;  
"Expression pattern and functional characteristics of two novel splice  
variants of the two-pore-domain potassium channel TREK-2.";  
J. Physiol. (Lond.) 539:657-668(2002).  
CC -I- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
activated by arachidonic acid and other naturally occurring  
unsaturated free fatty acids.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=A; Synonyms=TREK-2a;  
CC IsoId=P57789-1; Sequence=Displayed;  
CC Name=B; Synonyms=TREK-2b;  
CC IsoId=P57789-2; Sequence=VSP\_006697;  
CC Name=C; Synonyms=TREK-2c;  
CC IsoId=P57789-3; Sequence=VSP\_006698;  
CC -I- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney  
and to a lower level in brain, testis, colon, and small intestine.  
CC Isoform b is strongly expressed in kidney (primarily in the  
proximal tubule) and pancreas, whereas isoform c is abundantly  
expressed in brain.  
CC -I- SIMILARITY: Belongs to the two pore domain potassium channel  
(TC 1.A.1.8) family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).  
-----  
EMBL; AF279890; AAG15191.1; -;  
EMBL; AF385399; AAL95705.1; -;  
EMBL; AF385400; AAL95706.1; -;  
Genew; HGNC:6273; KCNK10.  
MIM; 605873; -;  
GO; GO:0005267; F:potassium channel activity; TAS.  
GO; GO:0006810; P:transport; TAS.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PR01333; 2FOREKCHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;  
KW Potassium; Potassium channel; Transmembrane; Transport;  
KW Voltage-gated channel.  
FT DOMAIN 1 71  
FT TRANSMEM 72 92 Cytoplasmic (Potential).  
FT DOMAIN 154 180 Pore-forming 1 (Potential).  
FT TRANSMEM 182 202 Potential.  
FT DOMAIN 203 233 Cytoplasmic (Potential).  
FT TRANSMEM 234 254 Potential.  
FT DOMAIN 263 294 Pore-forming 2 (Potential).  
FT TRANSMEM 299 319 Potential.  
FT DOMAIN 320 538 Cytoplasmic (Potential).  
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).  
FT VARSPIC 1 112 MFLFYTDFFLSL -> MKGDRTEGCRSDS (in isoform  
B).

FT VARSPLIC 1. 12 /FTID=VSP 006697.  
 FT MFLYTDFTSL -> MKPEIETPRKQVNDPK (in  
 FT isoform C).  
 FT /FTID=VSP 006698.  
 FT CONFLICT 529 529 E -> G (in Ref. 2).  
 SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 59.9%; Score 1251.5; DB 1; Length 538;  
 Best Local Similarity 64.3%; Pred. No. 2.3e-76;  
 Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADLLDPKSA-----AQNKPRLSPSSPTVLASRVESDS---AINVMKKTVSTI 50  
 DB 17 AAAPVQPKSATNGQPAPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKKTIVAI 75  
 QY 51 FLVVVLYLIGAAVFKALEQPOEISQRTTIVIQKOTFFIAQHACVNSTDELIIQIIVAAI 110  
 DB 76 FVVVVVLYTGLVFRALQEPPESSQKNTIALEKAEFLRHVCVSPQLETLIQHALDAD 135  
 QY 111 NAGIPLGNSSNQVSHWDLGSSFFPAGTIVTTIGFONISPRTEGKIFCIIIVALLGIPLF 170  
 DB 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCIIIVALLGIPLF 195  
 QY 171 GFLLAGVGDLGTIFGKIAKVEDTIFKWNVSQTKIRIISTIFILFGCVLFAVPAVIF 230  
 DB 196 GFLLAGIGDGLGTIFGKISARVEKVRKKQVSTKIRVISTILFILAGCIVFTIIPAVIF 255  
 QY 231 KHIEGWSALDAIFYFVVITLTITGFGDYVAGG-SDIEYLDYKPVVFWFVLVGLAYFAAVL 289  
 DB 256 KYIEGWTALESIYFVVVITLTITGFGDFVAGGNAGINREWKPLVWFWFVLVGLAYFAAVL 315  
 QY 290 SMIGDMLRVISKKTKEEVEGFRAHAAEWNTANTVTAEFKTRRLRSVEIYDKFORATSV--- 346  
 DB 316 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANTVTAEFRETRRLRSVEIHDKLORAATIRSM 375  
 QY 347 -KRKLSAELAGNHQELTPCRRTL 369  
 DB 376 ERRRLQDQRAHSLDMLSPKRSV 399

RESULT 12  
 Q68014 PRELIMINARY; PRT; 543 AA.  
 AC Q6B014;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE Potassium channel, subfamily K, member 10, isoform 3.  
 GN Name=KCNK10;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.

TISSUE=Pooled tissue;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton K., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Murzyn K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Pooled tissue;  
 RP Director MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC075022; AAH75022.1; -.  
 DR EMBL; BC075021; AAH75021.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005216; P:ion channel activity; IEA.  
 DR GO; GO:0005226; P:potassium channel activity; IEA.  
 DR GO; GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR011255; N1R\_S1ralpha\_1/3.  
 DR InterPro; IPR003976; Trek\_channel.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1499; TREKCHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;

Query Match 59.9%; Score 1251.5; DB 2; Length 543;  
 Best Local Similarity 64.3%; Pred. No. 2.3e-76;  
 Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADLLDPKSA-----AQNKPRLSPSSPTVLASRVESDS---AINVMKKTVSTI 50  
 DB 22 AAAPVQPKSATNGQPAPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKKTIVAI 80  
 QY 51 FLVVVLYLIGAAVFKALEQPOEISQRTTIVIQKOTFFIAQHACVNSTDELIIQIIVAAI 110  
 DB 81 FVVVVVLYTGLVFRALQEPPESSQKNTIALEKAEFLRHVCVSPQLETLIQHALDAD 140  
 QY 111 NAGIPLGNSSNQVSHWDLGSSFFPAGTIVTTIGFONISPRTEGKIFCIIIVALLGIPLF 170  
 DB 141 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCIIIVALLGIPLF 200  
 QY 171 GFLLAGVGDLGTIFGKIAKVEDTIFKWNVSQTKIRIISTIFILFGCVLFAVPAVIF 230  
 DB 201 GFLLAGIGDGLGTIFGKISARVEKVRKKQVSTKIRVISTILFILAGCIVFTIIPAVIF 260  
 QY 231 KHIEGWSALDAIFYFVVITLTITGFGDYVAGG-SDIEYLDYKPVVFWFVLVGLAYFAAVL 289  
 DB 261 KYIEGWTALESIYFVVVITLTITGFGDFVAGGNAGINREWKPLVWFWFVLVGLAYFAAVL 320  
 QY 290 SMIGDMLRVISKKTKEEVEGFRAHAAEWNTANTVTAEFKTRRLRSVEIYDKFORATSV--- 346  
 DB 321 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANTVTAEFRETRRLRSVEIHDKLORAATIRSM 380  
 QY 347 -KRKLSAELAGNHQELTPCRRTL 369  
 DB 381 ERRRLQDQRAHSLDMLSPKRSV 404

RESULT 13  
 Q68EY1 PRELIMINARY; PRT; 546 AA.  
 ID Q68EY1  
 AC Q68EY1;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE LOC446298 protein (Fragment).  
 GN Name=LOC446298;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RN SEQUENCE FROM N.A.



CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: AF248242; AAG31731.1; --  
 CC DR EMBL: AF247042; AAF64062.1; ALT\_INIT.  
 CC DR EMBL: AF259501; AAK49389.1; --  
 CC DR EMBL: AF259501; AAK49390.1; --  
 CC DR Genew: HGNC:6279; KCNK4.  
 CC MIM: 605720; --  
 CC GO: GO:005267; P:potassium channel activity; TAS.  
 CC GO: GO:006813; P:potassium ion transport; TAS.  
 CC DR InterPro: IPR003280; K+channel\_2pore.  
 CC DR InterPro: IPR001622; K+channel\_pore.  
 CC DR InterPro: IPR008074; TRAAK\_CHANNEL.  
 CC DR PRINTS: PRO1333; 2POREKCHANNEL.  
 CC DR PRINTS: PRO1691; TRAAKCHANNEL.  
 CC KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;  
 CC Potassium channel; Transmembrane; Transport;  
 CC Voltage-gated channel.  
 CC FT DOMAIN 1 3 Cytoplasmic (Potential).  
 CC FT TRANSMEM 4 24 Potential.  
 CC FT DOMAIN 89 113 Pore-forming 1 (Potential).  
 CC FT TRANSMEM 118 138 Potential.  
 CC FT DOMAIN 139 171 Cytoplasmic (Potential).  
 CC FT TRANSMEM 172 192 Potential.  
 CC FT DOMAIN 197 221 Pore-forming 2 (Potential).  
 CC FT TRANSMEM 234 254 Potential.  
 CC FT DOMAIN 255 393 Cytoplasmic (Potential).  
 CC FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).  
 CC FT VARSPIC 1 1 M -> MTPAQEPAPPLQAGSGAGPAPGRAM (in  
 CC isoform 2).  
 CC FT /FTID=VSP\_006689.  
 CC FT CONFLICT 328 328 P -> L (in Ref. 2).  
 CC SQ SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;

Query Match 38.1%; Score 797; DB 1; Length 393;  
 Best Local Similarity 51.1%; Pred. No. 8.1e-46;  
 Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;

QY 42 MKWKTSTPLVVVLLITGAAYKALEQPEISQRTTIVIOKTFIAOHACVNSTELDE 101  
 Db 1 MRSTLLALALLVLLVSGALVFRALQEPHEQQAQRELGVEKELRAHPCVSDQELGL 60  
 QY 102 LIQQIVAAINAGIPLGNSSNQVSH--WDLGSSFFPAGTVITITIGFNGISPRTEGGKIFC 159  
 Db 61 LIKEVADALGGGADPETNSTSSHSAMDLSGAFFSGTITITIGYGNVALRTDAGRLFC 120  
 QY 160 IYALLGIPFLGAGVDQIGTFKGIKVEDTFIKWVSQTKIRIISTIFILPGC 219  
 Db 121 IFYALVGIPFLGAGVDRLGSSLRHGIGIEAIFLKWHPPELVRLVLSAMFLFLIGC 180  
 QY 220 VLFVALPAVIEKHIEGWSALDIFYVITITIGFGDYVAGGSDIEYLDIFYKPVVWFLL-279  
 Db 181 LIFVLTPFTFCYMDWSKLEAIFYVITITVTFGFGDYVAGADPRDSPAYQPLVWFVLL 240  
 QY 280 VGLAYFAAVLSMGDWLRVLSKTKKEVGEFFRAHAAEWANTVTA 323  
 Db 241 LGLAYFASVLTITIGNLVRVSRTRAEKGLTQAASWTGTVTA 284

RESULT 15

CIW4\_MOUSE

ID\_CIW4\_MOUSE

AC 088454;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-  
 DE stimulated potassium channel protein) (TRAAK).  
 GN Name=Kcnk4; Synonyms=TRAAK;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98292450; PubMed=9628867; DOI=10.1093/emboj/17.12.3297;  
 RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,  
 RA Lazdunski M.;  
 RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and  
 RT polynsaturated fatty acids.";  
 RL EMBO J. 17:3297-3308(1998).  
 RN [2]  
 RP ACTIVATION  
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K+  
 RT channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -!- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying  
 CC potassium channel. Outward rectification is reversed at high  
 CC external K(+) concentrations.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O88454-1; Sequence=Displayed;  
 CC Name=2; Synonyms=TRAAK, Truncated;  
 CC IsoId=O88454-2; Sequence=VSP\_006690, VSP\_006691;  
 CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not  
 CC detected in heart, skeletal muscle, liver, lungs, kidney and  
 CC testis.  
 CC -!- MISCELLANEOUS: Activated by arachidonic acid and other unsaturated  
 CC fatty acids. Not affected by volatile general anaesthetics such as  
 CC chloroform, diethyl ether, halothane and isoflurane.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: AF056492; AAC40181.1; --  
 CC DR MGD; MGI:1298234; Kcnk4.  
 CC DR InterPro: IPR003280; K+channel\_2pore.  
 CC DR InterPro: IPR001622; K+channel\_pore.  
 CC DR InterPro: IPR008074; TRAAK channel.  
 CC DR PRINTS: PRO1333; 2POREKCHANNEL.  
 CC DR PRINTS: PRO1691; TRAAKCHANNEL.  
 CC KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;  
 CC Potassium channel; Transmembrane; Transport;  
 CC Voltage-gated channel.  
 CC FT DOMAIN 1 3 Cytoplasmic (Potential).  
 CC FT TRANSMEM 4 24 Potential.  
 CC FT DOMAIN 89 113 Pore-forming 1 (Potential).  
 CC FT TRANSMEM 119 139 Potential.  
 CC FT DOMAIN 140 171 Cytoplasmic (Potential).  
 CC FT TRANSMEM 172 192 Potential.  
 CC FT DOMAIN 198 222 Pore-forming 2 (Potential).  
 CC FT TRANSMEM 235 255 Potential.  
 CC FT DOMAIN 256 398 Cytoplasmic (Potential).  
 CC FT CARBOHYD 81 81 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 84 84 N-linked (GlcNAc...) (Potential).  
 CC FT VARSPIC 63 67 KLLVE -> KAWAI (in isoform 2).



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:02:40 ; Search time 21.6316 Seconds  
(without alignments)  
1828.118 Million cell updates/sec

Title: US-09-503-089A-4  
Perfect score: 2090  
Sequence: 1 MAAPLLDPKSAQNSKPL.....LNLTPHCAGSDIAVIENMK 411  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	376.5	18.0	336	2 S65566	inward rectifier
2	351.5	16.8	330	2 JC7703	TASK-5 protein - h
3	343	16.4	329	2 T43509	probable potassium
4	329.5	15.8	336	2 T32347	outward rectifier
5	325	15.6	1001	2 T13807	potassium channel
6	289	13.8	383	2 T23182	hypothetical prote
7	286.5	13.7	334	2 T19860	hypothetical prote
8	286.5	13.7	364	2 T43361	probable potassium
9	279.5	13.4	461	2 T43394	potassium channel
10	279	13.3	393	2 T23392	hypothetical prote
11	271	13.0	392	2 T45032	hypothetical prote
12	270.5	12.9	522	2 T24265	hypothetical prote
13	269	12.9	325	2 T15584	hypothetical prote
14	266	12.7	1910	2 H88124	protein T129_3 [i
15	263	12.6	452	2 T21118	hypothetical prote
16	252.5	12.1	1539	2 T30037	hypothetical prote
17	247	11.8	444	2 T26229	hypothetical prote
18	245.5	11.7	513	2 T28933	hypothetical prote
19	243.5	11.7	427	2 T27681	hypothetical prote
20	237	11.3	643	2 T26616	hypothetical prote
21	236	11.3	550	2 T29557	hypothetical prote
22	231	11.1	524	2 T23907	hypothetical prote
23	229.5	11.0	484	2 T43529	probable potassium
24	229.5	11.0	519	2 T16529	hypothetical prote
25	229	11.0	528	2 T21834	hypothetical prote
26	221	10.6	443	2 T21598	hypothetical prote
27	219	10.5	1136	2 T28953	hypothetical prote
28	217	10.4	691	2 S4585	outward-rectifier
29	216.5	10.4	551	2 T16426	hypothetical prote

30	216.5	10.4	555	2 T43357	potassium channel
31	216	10.3	475	2 T27725	hypothetical prote
32	215.5	10.3	335	2 S44635	f22b7.7 protein -
33	212	10.1	307	2 H89074	protein twk-24 [im
34	212	10.1	485	2 T24201	hypothetical prote
35	209.5	10.0	586	2 T21683	hypothetical prote
36	206.5	9.9	660	2 T21551	hypothetical prote
37	205	9.8	700	2 T27364	hypothetical prote
38	204.5	9.8	523	2 T23373	hypothetical prote
39	204.5	9.8	544	2 T43364	potassium channel
40	204.5	9.8	576	2 T43363	potassium channel
41	202.5	9.7	769	2 T27550	hypothetical prote
42	199.5	9.5	539	2 T23700	hypothetical prote
43	196.5	9.4	681	2 T19429	hypothetical prote
44	194.5	9.3	569	2 T43531	probable potassium
45	192.5	9.2	381	2 T43393	potassium channel

ALIGNMENTS

RESULT 1

S65566  
inward rectifier potassium channel TWIK-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S65566  
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMO J. 15, 1004-1011, 1996  
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel A:Reference number: S65566; MUID:96183184; PMID:8605869  
A:Accession: S65566  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-336 <LES>  
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g10

Query Match 18.0%; Score 376.5; DB 2; Length 336;  
Best Local Similarity 32.5%; Pred. No. 6.3e-23;  
Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY	51	FLVV--VLIIIGAAVFALEQOEISQRTTIVIQKTFIAQHACVNSTELDLIIQIIVA	108
DB	25	FLVGLYLLVFGAVVFSVELPYEDLLRQELKLRFRLEBHECLSEQOLEQFLGRVLE	84
QY	109	AINAGIPIIIGNSNOVSHWDLGSSFFFACTVITIGFNGISPRTEGGKIFCIYALLGIP	168
DB	85	ASNYGVSVLSNASGN-WNWDFTSALFFASTVLTGTYGHTVPLSDGGKAFCIYISVIGIP	143
QY	169	LFGFLLAGVGDQLGTFIFGKGIARVEDTFIKMNVSTQKIRIISTII--FILFGCVLPVALP	226
DB	144	FTLLFLTAVVQRITVHVTR--RPVLVPHIRMGFSKQVVAIHAVLGGFVTVSCFFFI--P	199
QY	227	AVIFKHIE-GWSALDAIFVWITLTITIGFDYVAG-GSDIEYLDYFKVPVWFVWILGLAY	284
DB	200	AAVFSVLEDDWNFLSFYFCFISLTIGLDYVPGEYGNQKPRELYKIGITCYLLGLLIA	259
QY	285	FAAVLSMIGDLRLVTSK-----KTKEEVEGFRAHAAE	316
DB	260	MLVLETFCF-LHELKKFRKFMFYVKDDEQVHIIE	295

RESULT 2

JC7703  
TASK-5 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: JC7703  
R:Kim, D.; Gnatenco, C. Biochem. Biophys. Res. Commun. 284, 923-930, 2001  
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.  
A:Reference number: JC7703; MUID:21303050; PMID:11409881  
A:Accession: JC7703







Query Match 15.6%; Score 325; DB 2; Length 1001;  
Best Local Similarity 28.8%; Pred. No. 3.5e-18;  
Matches 90; Conservative 62; Mismatches 125; Indels 36; Gaps 10;

QY 50 IFVLVVLIIIGAAVFKALEQOE-----ISQRTTIVIQKTFIAQHACVNSTELDELIOQ 105  
DB 9 LLIFYSYLMFAGAAIYHEGEEKISRAEQAKAIANEYILLELGDKNTTQDEILQR 68

QY 106 IVAANAGIPIPLGSSNQVSHDLGSSFFPAGVTITIGFNGISPRTEGKIFCIYALL 165  
DB 69 ISDYCDKPVTLPTTDDTYTTFYHAFPAFTVSTVGYNISPTTFAGRMIMATYSVI 128

QY 166 GIPLFGFLAGVDQGLTFPGKIAKVEDTFIKMNV-----OTKIRIISTIFILF-G 218  
DB 129 GIPVNGILFAG---LGEYFGRTFEAIYRRYKXKXMTDMHVVPQGLITTVIALIPG 184

QY 219 CVLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYVA-----GSDIEYLD 268  
DB 185 IALFLLPSWVTFYFENWPYSISLYSYVTITITIGFDYVPTFGANQPKFEGGVVYQI 244

QY 269 FYKPVVFWILVGLAYFAAVALSMIGDMLRVISKK---TKEEVGFRAHAAEWTANVTAE 324  
DB 245 FV--IWP--IFSGLVLMWMTFIRGLQ--SKLAYLEQQLSSNLKATQNRWISGVTKD 298

QY 325 FKETRRLSVEIY 337  
DB 299 VGYLRMLN-ELY 310

RESULT 6  
T23182  
Hypothetical protein K01D12.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T23182  
R:Dobson, R.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19703  
A:Accession: T23182  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-383 <WIL>  
A:Cross-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4  
A:Experimental source: clone K01D12  
C:Genetics:  
A:Gene: CESP:K01D12.4  
A:Map position: 5  
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 13.8%; Score 289; DB 2; Length 383;  
Best Local Similarity 24.2%; Pred. No. 9.2e-16;  
Matches 88; Conservative 80; Mismatches 122; Indels 74; Gaps 14;

QY 15 NSKPLSPSKPTVLASRVESDSAINVMKWTSTIFLVVLYLIIGAAVFKALEQOE 74  
DB 19 NTLPSITRAKVGCFARLRIYEENARFV-----ICILIVLAPGAILFHWLEWNEV 71

QY 75 SORTTI---VIOKQTFIAQHACVNSTELDELIOQIVAAINAGIPIPLGSSNQVSHDLG 131  
DB 72 DERIAIDNRADYQKYVCKHKLNECDPEEMVRFISDGTSGLL---NSRSRFDH--LG- 125

QY 132 SPFFAGTITITIGFNGISPRTEGKIFCIYALLG---IPLFGFLAGVDQGLTFPGK 187  
DB 126 SLFFSATVISTIGFNGISPRTEGKIFCIYALLG---IPLFGFLAGVDQGLTFPGK 181

QY 188 GIAKVEDTFIKNVSTQKIRIISTII-----FILFG-C 219  
DB 182 ILRSLFERKIRYRLKESGKNPVTLLNNEDEFNSSSCGHHMDNRPSYKVFILFSC 241

QY 220 VLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYL---DPKPVVFW 277  
DB 242 LVLITASAGIYVVENWNYIDSLYFCISFATIGFDYVSNQDVTMRSPDLYRFVNFCL 301

QY 278 ILVGLAYF-----AAVLSMIGDMLRVISKTKKEEVEGFRAHAAEWTANVTAEKETR 330  
DB 302 LTLGACFFVCLSNVSSIVVRQLLNMW---IKQMDVKV-EDRSFLC-----FKKRR 348

QY 331 RLSV 334  
DB 349 YNGL 352

RESULT 7  
T19860  
Hypothetical protein C40C9.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T19860  
R:Hembry, C.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19188  
A:Accession: T19860  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-334 <WIL>  
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1  
A:Experimental source: clone C40C9  
C:Genetics:  
A:Gene: CESP:C40C9.1  
A:Map position: X  
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 13.7%; Score 286.5; DB 2; Length 334;  
Best Local Similarity 28.7%; Pred. No. 1.3e-15;  
Matches 90; Conservative 58; Mismatches 113; Indels 53; Gaps 12;

QY 50 IFVLVVLIIIGAAVFKALEQOEISQRTTIV---IQKTFIAQHACVNSTELDELIOQ 106  
DB 14 LILSTFTYLLFGAMVFDKLE-----SEKDTWRDIERITDLKHK-YNFSERD---LHL 64

QY 107 VAAINAGIPIPLGSSNQVSH-WDLGSSFFPAGVTITIGFNGISPRTEGKIFCIYALL 165  
DB 65 FEAIKISIP-----QQAGYQWQFAGAFVATVITTVGYGHSAPSTNAGKLFMIFALF 119

QY 166 GIPLFGFLAGVDQGLTFPGKIAKVEDTFIK-----WNVSTQKIRIIS-TIIFILFG 218  
DB 120 GYPMGLIMFQIGERVNTFIAYSLHFRDSLHQOQFTCLQEVTPTHLLMVSLTIGFMV-- 177

QY 219 CVLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYV--AGGSDIEYLDYFKPVVWF 276  
DB 178 ----IVSGTYMHTTEKWSIPDAYIFCMITFTIGDLPVLPQQVNALQDQLYVPATIM 233

QY 277 WILVGLAYFAAVALSMIGDMLRVISKTKKEEVEGFRAHAAEWTANVTAEKETRRLSVEI 336  
DB 234 FILGLAVFSACVNL-----VLGFMASNADEVTA-----AQREPPSAIV 273

QY 337 YDKFORATSVKRL 350  
DB 274 LERFTRNSLVDSQI 287

RESULT 8  
T43361  
Probable potassium channel chain n2P20 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T43361  
R:Wang, Z.W.; Salkoff, L.  
submitted to the EMBL Data Library, August 1998  
A:Description: Potassium channels in C. elegans.  
A:Reference number: Z22450  
A:Accession: T43361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-364 <WAN>



A;Reference number: S43531; MUID:94150718; PMID:7906398  
A;Accession: T45032  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-392 <WIL>  
A;Cross-references: EMBL:AL132896; NID:G6434440; PIDN:G6434446  
A;Experimental source: clone Y39B6B  
C;Genetics:  
A;Map position: 3  
A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
A;Note: Y39B6B.f

Query Match 13.0%; Score 271; DB 2; Length 392;  
Best Local Similarity 25.8%; Pred. No. 2.7e-14;  
Matches 82; Conservative 65; Mismatches 109; Indels 62; Gaps 12;

QY 7 LDPKSAQNS-----KPLSFSSKPTVLAS---RVESDSAINVMKWTSTIFLVVLY 57  
DB 64 LEPTSAHSSLYPVEPKIAKEMSFYDQKPKFHFHFFSLKISKLPKAKRY----- 117

QY 58 LIIGAAYFKALEQOEISORTTIVIQOTPIAQ--HACVNSTELDELIQOI--VAAINAGI 114  
DB 118 -----FSRIEYPLEKIEREAYLDYQNMQRDLIQLDIDSEIDKPLNIREAALNG-- 168

QY 115 IPLGNSSNQSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGPIPLFGFL 174  
DB 169 IWMRNLTSDPNWFQAFQAFAGTILSTVGYGRVSPRTBYGKLTILYCVIGIPLTLALL 228

QY 175 AGV-----GDQLTIFGKIAKVEDFFIKWNVSTQKIRIISTIFILFGC 219  
DB 229 SAIVARMRPSHKRLGMLNORLGHF-----TVNHIQLHVGCV-VFASL 271

QY 220 VLVF-ALPAPVIFKHIE-GWSALDAIYFVVTITTTIGFGDYVAGGS-DIBYLDYFKPVWF 276  
DB 272 LIFVFAIPAWVFSSITDSYLDIFYCYFSLTTLIGLDFEPGDDNQSPRGYKIGATV 331

QY 277 WILVGLAYFAAVLSMTGD 294  
DB 332 YLMGGLCCMMLFLATLYD 349

RESULT 12  
T24265  
hypothetical protein T01B4.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T24265  
R;Wilkinson, J.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z19866  
A;Accession: T24265  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-522 <WIL>  
A;Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4  
A;Experimental source: clone T01B4  
C;Genetics:  
A;Gene: CESP.T01B4.1  
A;Map position: X  
A;Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.9%; Score 270.5; DB 2; Length 522;  
Best Local Similarity 23.7%; Pred. No. 4.2e-14;  
Matches 102; Conservative 64; Mismatches 136; Indels 129; Gaps 15;

QY 50 IFLVVLYLIIGAAVFKALEQOE-----ISQRTTIVIQOTPIAQHACVNSTE 98  
DB 41 LILILGYACLGGMFQALEYDQOLEAEKRVLSSESLLANVLLHLKOMNCQSQSNE 100

QY 99 LDELIQOIVAINAGIIPIGNSS-NQVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKI 157  
DB 101 -----KRCLELITPTQISDEERGWRWDFWNSVFFSATIPTTTIGYGNLACKNLGRI 155

QY 158 FCIIVALLGIPPLFGELLACVGD-----QLGTIFGKG 188  
DB 156 ATIIYIGMIGLMLFVLKFNFGELCKVMAKKIOFNVOOCLKCFGRKQKASSLASITSE 215

QY 189 IAKV-----EDTF--IKNVSTQKIRIISTIFILFGCVLFAVPAVIFKHIEGWS 237  
DB 216 MLEVFEVPEDDKEDTTFQLRWG-----LLVIVLFFVLCSFVVSFWENWD 260

QY 238 ALDAIYFVVTITTTIGFGDYVAGGSIDIEYLDYFKPVVWFIL--VGLAYFAAVLSMTGD- 294  
DB 261 PUTAPYFPFVSLSTIGFGDIVP-----DHPRTACALFVLVFIGLAFAMVYAILQER 312

QY 295 -----W-LRVISKTKBEVGEFRAHAAEWANVT----- 322  
DB 313 VENQYMWALLELDQYOEKLDQMDYDEDEKADKNDMHFSKKEPVGRGPRILLQDLLRGPD 372

QY 323 ASFEKTRRLS-----VEIYDKFORATSVKKEKLSAEL-----AGNHQELTPCRRTLS 370  
DB 373 LKISGRSSSSDASSVITEASDEDTRFVKVGRAILAEAFAPDERASNHGTQNSC--TVS 430

QY 371 VNHLTSEREVL 381  
DB 431 NEHDSQOIEAI 441

RESULT 13  
T15584  
hypothetical protein C24A3.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T15584  
R;Favvello, T.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid C24A3.  
A;Reference number: Z18373  
A;Accession: T15584  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-325 <FAV>  
A;Cross-references: EMBL:U40424; NID:G1065542; PID:G1065543; PIDN:AAA81455.1; CESP:C24A3.6  
A;Gene: CESP:C24A3.6  
A;Introns: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match 12.9%; Score 269; DB 2; Length 325;  
Best Local Similarity 25.4%; Pred. No. 3.2e-14;  
Matches 87; Conservative 53; Mismatches 87; Indels 116; Gaps 11;

QY 46 TVSTIF-----LVVLYLIIGAAVFKALEQOEISQRTTIVIQOTPIAQHACVN 95  
DB 10 TILTTFTQKTFKGLLPLIILVAYTLGAWTFWMIEGENE---REMLTEQOK----- 56

QY 96 STELDELIOQIVAAIN-----AGIIPLGNSSNOVS 125  
DB 57 ---ERDELIRRTYKINQIKQRRLMTABEENYNTAKVLTFTFQETLGIIPA--DMDKDI 112

QY 126 HMDLGSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGPIPLFGLLAGVDQLGTIF 185  
DB 113 HMTFLGSIFYCMVTVTYTTIGYGNIVPTCGWGRFATILYAFIGIPLTVLSLY----CLGSUF 168

QY 186 GKGIKAVEDTFIKWNVSTQKIRIIS----- 210  
DB 169 AKGCKMLRFFLK-----STRVSKDLSNKISEAADNIEEGTATTTPSAEKTENNDDDL 222

QY 211 ---TIIFILFGCVLFAVPAVIFKHIEGWSALDAIYFVVTITTTIGFGDYVAGGSIDIEYL 267  
DB 223 LSPFISGLLITIVIWIFCAVLFTLEEDWDFGTSYFTLISFTTIGFGDILP--SDYDEM 280

QY 268 DPKVPWFVWILVGLAYFAAVLSMTGDMLRVIS-----KKTKE 305  
DB 281 ----FIVGVLLIIGLSLSTVMTLIIQQOIEALASVRRRRKKKK 319



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 90.2442 Seconds  
(without alignments)  
1759.475 Million cell updates/sec

Title: US-09-503-089A-4  
Perfect score: 2090  
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNLTPHCAGEDIAVNIENK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*  
23: /cgn2\_6/ptodata/1/pubpaa/US12\_PUBCOMB.pep.\*  
24: /cgn2\_6/ptodata/1/pubpaa/US12\_NEW\_PUB.pep.\*  
25: /cgn2\_6/ptodata/1/pubpaa/US12\_PUBCOMB.pep.\*  
26: /cgn2\_6/ptodata/1/pubpaa/US13\_PUBCOMB.pep.\*  
27: /cgn2\_6/ptodata/1/pubpaa/US13\_NEW\_PUB.pep.\*  
28: /cgn2\_6/ptodata/1/pubpaa/US13\_PUBCOMB.pep.\*  
29: /cgn2\_6/ptodata/1/pubpaa/US14\_PUBCOMB.pep.\*  
30: /cgn2\_6/ptodata/1/pubpaa/US14\_NEW\_PUB.pep.\*  
31: /cgn2\_6/ptodata/1/pubpaa/US14\_PUBCOMB.pep.\*  
32: /cgn2\_6/ptodata/1/pubpaa/US15\_PUBCOMB.pep.\*  
33: /cgn2\_6/ptodata/1/pubpaa/US15\_NEW\_PUB.pep.\*  
34: /cgn2\_6/ptodata/1/pubpaa/US15\_PUBCOMB.pep.\*  
35: /cgn2\_6/ptodata/1/pubpaa/US16\_PUBCOMB.pep.\*  
36: /cgn2\_6/ptodata/1/pubpaa/US16\_NEW\_PUB.pep.\*  
37: /cgn2\_6/ptodata/1/pubpaa/US16\_PUBCOMB.pep.\*  
38: /cgn2\_6/ptodata/1/pubpaa/US17\_PUBCOMB.pep.\*  
39: /cgn2\_6/ptodata/1/pubpaa/US17\_NEW\_PUB.pep.\*  
40: /cgn2\_6/ptodata/1/pubpaa/US17\_PUBCOMB.pep.\*  
41: /cgn2\_6/ptodata/1/pubpaa/US18\_PUBCOMB.pep.\*  
42: /cgn2\_6/ptodata/1/pubpaa/US18\_NEW\_PUB.pep.\*  
43: /cgn2\_6/ptodata/1/pubpaa/US18\_PUBCOMB.pep.\*  
44: /cgn2\_6/ptodata/1/pubpaa/US19\_PUBCOMB.pep.\*  
45: /cgn2\_6/ptodata/1/pubpaa/US19\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2084	99.7	411	9 US-09-828-746-6	Sequence 6, Appl1
2	2044	97.8	411	9 US-09-828-746-2	Sequence 2, Appl1
3	2044	97.8	411	14 US-10-121-746-83	Sequence 83, Appl1
4	2044	97.8	411	16 US-10-121-746-2	Sequence 2, Appl1
5	2044	97.8	411	16 US-10-349-528-31	Sequence 31, Appl1
6	2044	97.8	411	17 US-10-976-644-83	Sequence 83, Appl1
7	2044	97.8	411	17 US-10-976-644-83	Sequence 83, Appl1
8	2041	97.7	411	11 US-09-892-360-18	Sequence 18, Appl1
9	2038	97.5	422	16 US-10-349-528-20	Sequence 20, Appl1
10	2011	96.2	426	8 US-08-816-011-45	Sequence 45, Appl1
11	2011	96.2	426	17 US-10-870-492-45	Sequence 45, Appl1

12	2007	96.0	426	17	US-10-870-492-57	Sequence 57, Appl1
13	2006	96.0	426	17	US-10-870-492-58	Sequence 58, Appl1
14	2003	95.8	426	17	US-10-870-492-60	Sequence 60, Appl1
15	2002	95.8	426	17	US-10-870-492-59	Sequence 59, Appl1
16	1855	88.8	370	9	US-09-939-484-8	Sequence 8, Appl1
17	1855	88.8	370	9	US-09-939-483-8	Sequence 8, Appl1
18	1256.5	60.1	538	9	US-09-729-920-5	Sequence 5, Appl1
19	1256.5	60.1	538	16	US-10-887-932-5	Sequence 5, Appl1
20	1251.5	59.9	526	9	US-09-729-920-4	Sequence 4, Appl1
21	1251.5	59.9	526	16	US-10-887-932-4	Sequence 4, Appl1
22	1251.5	59.9	538	11	US-09-892-360-2	Sequence 2, Appl1
23	1251.5	59.9	538	18	US-10-923-035-46	Sequence 46, Appl1
24	1251.5	59.9	543	9	US-09-729-920-2	Sequence 2, Appl1
25	1251.5	59.9	543	10	US-09-852-386-73	Sequence 73, Appl1
26	1251.5	59.9	543	14	US-10-332-175-2	Sequence 2, Appl1
27	1251.5	59.9	543	15	US-10-262-511-106	Sequence 106, Appl1
28	1251.5	59.9	543	16	US-10-887-932-2	Sequence 2, Appl1
29	1224	58.6	724	15	US-10-332-447-10	Sequence 10, Appl1
30	797	38.1	392	9	US-09-747-835A-55	Sequence 55, Appl1
31	797	38.1	392	15	US-10-312-312-55	Sequence 55, Appl1
32	797	38.1	393	14	US-10-243-035-2	Sequence 2, Appl1
33	797	38.1	419	9	US-09-828-035-2	Sequence 2, Appl1
34	797	38.1	419	14	US-10-345-680-44	Sequence 44, Appl1
35	797	38.1	419	14	US-10-146-733-29	Sequence 29, Appl1
36	797	38.1	419	15	US-10-352-684A-8	Sequence 8, Appl1
37	797	38.1	419	15	US-10-391-399-19	Sequence 19, Appl1
38	797	38.1	419	16	US-10-768-158-12	Sequence 12, Appl1
39	797	38.1	481	18	US-10-852-707-65	Sequence 65, Appl1
40	797	38.1	822	18	US-10-852-707-64	Sequence 64, Appl1
41	797	38.1	1314	9	US-09-747-835A-29	Sequence 29, Appl1
42	797	38.1	1314	15	US-10-312-312-29	Sequence 29, Appl1
43	770.5	36.9	398	11	US-09-892-360-19	Sequence 19, Appl1
44	726	34.7	924	18	US-10-852-707-66	Sequence 66, Appl1
45	726	34.7	1125	18	US-10-852-707-60	Sequence 60, Appl1

ALIGNMENTS

RESULT 1  
US-09-828-746-6  
; Sequence 6, Application US/09828746  
; Patent No. US20020028485A1  
; GENERAL INFORMATION:  
; APPLICANT: Helen Jane Meadows  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30031-D1  
; CURRENT APPLICATION NUMBER: US/09/828,746  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 09/236,080  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: EP 98300570.3  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: UK 9822135.1  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-828-746-6

Query Match	99.7%	Score	2084	DB	9	Length	411
Best Local Similarity	99.8%	Pred. No.	5.5e-189				
Matches	410	Conservative	0	Mismatches	1	Indels	0
		Gaps	0				
QY	1	MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTFIFLVVLYLI	60				
Db	1	MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTFIFLVVLYLI	60				
QY	61	GAAPFKALEPQOEISQRTTIVIQKFTTFAQAACVNSTELDELIIQIVAAINAGIPLGNS	120				

```
Db 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
```

## RESULT 2

```
US-09-828-746-2
; Sequence 2, Application US/09828746
; Publication No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2
```

```
Query Match 97.8%; Score 2044; DB 9; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIVLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIVLVVLYLII 60
QY 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
Db 61 GATVFKALEQPOHEISQRTTIVIKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 120
QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
```

```
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 411
```

## RESULT 3

```
US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83
```

```
Query Match 97.8%; Score 2044; DB 14; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIVLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIVLVVLYLII 60
QY 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
Db 61 GATVFKALEQPOHEISQRTTIVIKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 120
QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFILFGCVLFVALPVAIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 411
```

## RESULT 4

```
US-10-745-210-2
; Sequence 2, Application US/10745210
; Publication No. US20040143855A1
; GENERAL INFORMATION:
; APPLICANT: TONONI, Giulio
; APPLICANT: CIRELLI, Chiara
; TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
; FILE REFERENCE: 054030-0044
; CURRENT APPLICATION NUMBER: US/10/745,210
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,201
; PRIOR FILING DATE: 2001-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-745-210-2

Query Match          97.8%; Score 2044; DB 16; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
QY 61 GAAVFKALQPOEISORTTIVIQKQTFIAQHACVNSTELDELQOIVAAINAGIIPLGNS 120
DB 61 GATVFKALQPOEISORTTIVIQKQTFISQHCVCNSTELDELQOIVAAINAGIIPLGNT 120
QY 121 SNQVSHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGHSALD 240
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGHSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWVWVWVWVWVWVWVWVWVWVWVWV 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWVWVWVWVWVWVWVWVWVWVWV 300
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLKLSAELAGNHQ 360
DB 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLKLSAELAGNHQ 360
QY 361 ELTPCRTLTVSNHLSERVLPLPKAESIYNGLTPHCAGEDIAVIENMK 411
DB 361 ELTPCRTLTVSNHLSERVLPLPKAESIYNGLTPHCAGEDIAVIENMK 411

RESULT 5
US-10-349-528-31
; Sequence 31, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE REFERENCE: D0210
; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
```

```
US-10-349-528-31

Query Match          97.8%; Score 2044; DB 16; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
QY 61 GAAVFKALQPOEISORTTIVIQKQTFIAQHACVNSTELDELQOIVAAINAGIIPLGNS 120
DB 61 GATVFKALQPOEISORTTIVIQKQTFISQHCVCNSTELDELQOIVAAINAGIIPLGNT 120
QY 121 SNQVSHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGHSALD 240
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGHSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWVWVWVWVWVWVWVWVWVWVWV 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWVWVWVWVWVWVWVWVWVWVWV 300
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLKLSAELAGNHQ 360
DB 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLKLSAELAGNHQ 360
QY 361 ELTPCRTLTVSNHLSERVLPLPKAESIYNGLTPHCAGEDIAVIENMK 411
DB 361 ELTPCRTLTVSNHLSERVLPLPKAESIYNGLTPHCAGEDIAVIENMK 411

RESULT 6
US-10-976-644-83
; Sequence 83, Application US/10976644
; Publication No. US20050112662A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURRAN, Mark Edward
; APPLICANT: HU, Ping
; APPLICANT: RUTTER, Marc
; APPLICANT: WANG, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,644
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-976-644-83

Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
```



QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120  
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
QY 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240  
DB 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240  
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
QY 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411  
DB 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411

## RESULT 7

US-10-976-647-83  
; Sequence 83, Application US/10976647  
; Publication No. US20050112663A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: Novel Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/976,647  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/336,643  
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-10-976-647-83

Query Match 97.8%; Score 2044; DB 17; Length 411;  
Best Local Similarity 96.4%; Pred. No. 3.5e-185;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTPTVLASRVESDTINVMKWTSTIFLVVLYLII 60  
QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120  
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
QY 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240  
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
QY 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411  
DB 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411

## RESULT 8

US-09-892-360-18  
; Sequence 18, Application US/09892360  
; Publication No. US20040101833A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: ROMEO, GEORGES  
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
; TITLE OF INVENTION: RILUZOLE  
; FILE REFERENCE: 1256-R-00  
; CURRENT APPLICATION NUMBER: US/09/892,360  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 60/214,559  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-892-360-18

Query Match 97.7%; Score 2041; DB 11; Length 411;  
Best Local Similarity 96.1%; Pred. No. 6.7e-185;  
Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTPTVLASRVESDTINVMKWTSTIFLVVLYLII 60  
QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120  
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120  
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIFLPGFLLAGVGQD 180  
QY 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240  
DB 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTITFIIFLFGCVLFVALPAVIFKHIEGWSALD 240  
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDWLRVIS 300  
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360  
QY 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411  
DB 361 ELTPCRRTLSVNHLTSEREVLPLPKAESIYVNGLTTPHCAGEDIAVIENMK 411

## RESULT 9





```
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-45

Query Match          96.2%; Score 2011; DB 17; Length 426;
Best Local Similarity 95.1%; Pred. No. 5e-182;
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVSDSAINVMKWKTVSTIFLVVLYLII 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTVSTIFLVVLYLII 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAAVFKALEQPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVNSTELDELIQQIVAAINAGIIPLGNT 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLFGLAGVGDQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLFGLAGVGDQ 195
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LGTIFGKGIKVEDTEFIKWNVSQTKIRIISTIIIFLFCVLFVALPAVIFKHIEGWSALD 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTEFIKWNVSQTKIRIISTIIIFLFCVLFVALPAVIFKHIEGWSALD 255
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAFLSMIGDMLRVIS 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 TIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAFLSMIGLVRVIS 315
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 KKTKEEVGEFRAHAAEWANTVTAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 360
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEEVGEFRAHAAEWANTVTAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 375
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 ELTPCRRTLSVNHLTSREVLPLLKASIIYLANGITPHCAGEDIAVIENMK 411
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSREVLPLLKASIIYLANGITPHCAGEDIAVIENIK 426
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-870-492-58
; Sequence 58, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-58

Query Match          96.0%; Score 2006; DB 17; Length 426;
Best Local Similarity 94.9%; Pred. No. 1.5e-181;
Matches 390; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVSDSAINVMKWKTVSTIFLVVLYLII 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTVSTIFLVVLYLII 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAAVFKALEQPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVNSTELDELIQQIVAAINAGIIPLGNT 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLFGLAGVGDQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLFGLAGVGDQ 195
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LGTIFGKGIKVEDTEFIKWNVSQTKIRIISTIIIFLFCVLFVALPAVIFKHIEGWSALD 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTEFIKWNVSQTKIRIISTIIIFLFCVLFVALPAVIFKHIEGWSALD 255
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAFLSMIGDMLRVIS 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 TIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAFLSMIGLVRVIS 315
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 KKTKEEVGEFRAHAAEWANTVTAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 360
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEEVGEFRAHAAEWANTVTAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 375
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 ELTPCRRTLSVNHLTSREVLPLLKASIIYLANGITPHCAGEDIAVIENMK 411
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSREVLPLLKASIIYLANGITPHCAGEDIAVIENIK 426
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-870-492-57
; Sequence 57, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-57

Query Match          96.0%; Score 2007; DB 17; Length 426;
Best Local Similarity 94.9%; Pred. No. 1.2e-181;
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
```

Db 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLVALPAIIFKHIEGWSALD 255  
Qy 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300  
Db 256 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGRLVRVIS 315  
Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 360  
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 375  
Qy 361 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411  
Db 376 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426  
RESULT 14  
US-10-870-492-60  
; Sequence 60, Application US/10870492  
; Publication No. US20050032165A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUSCH, MARK H.  
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/10/870,492  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/503,849  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR FILING DATE: 1995-10-25  
; PRIOR FILING DATE: 1994-10-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-870-492-60  
Query Match 95.8%; Score 2003; DB 17; Length 426;  
Best Local Similarity 94.9%; Pred. No. 2.9e-181;  
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDSAINVMKTKVSTIFLWVLYLII 60  
Db 16 VAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKTKVSTIFLWVLYLII 75  
Qy 61 GAAVFKALEQPOEISORTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120  
Db 76 GATVFKALEQPOHEISORTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 135  
Qy 121 SNQVSHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPILFGFLLAGVGQD 180  
Db 136 SNQISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPILFGFLLAGVGQD 195  
Qy 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLVALPAIIFKHIEGWSALD 240  
Db 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLVALPAIIFKHIEGWSALD 255  
Qy 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300  
Db 256 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGRLVRVIS 315  
Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 360  
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 375  
Qy 361 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411  
Db 376 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426

Search completed: July 13, 2005, 09:07:01  
Job time : 91.2442 secs

Db 376 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426  
RESULT 15  
US-10-870-492-59  
; Sequence 59, Application US/10870492  
; Publication No. US20050032165A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUSCH, MARK H.  
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/10/870,492  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/503,849  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR FILING DATE: 1995-10-25  
; PRIOR FILING DATE: 1994-10-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-870-492-59  
Query Match 95.8%; Score 2002; DB 17; Length 426;  
Best Local Similarity 94.6%; Pred. No. 3.6e-181;  
Matches 389; Conservative 14; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDSAINVMKTKVSTIFLWVLYLII 60  
Db 16 VAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKTKVSTIFLWVLYLII 75  
Qy 61 GAAVFKALEQPOEISORTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120  
Db 76 GATVFKALEQPOHEISORTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 135  
Qy 121 SNQVSHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPILFGFLLAGVGQD 180  
Db 136 SNQISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPILFGFLLAGVGQD 195  
Qy 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLVALPAIIFKHIEGWSALD 240  
Db 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLVALPAIIFKHIEGWSALD 255  
Qy 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGDMLRVIS 300  
Db 256 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVALSMIGRLVRVIS 315  
Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 360  
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRKLSAELAGNHQ 375  
Qy 361 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411  
Db 376 ELTPCRRTLSVNHLSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds  
(without alignments)  
1163.760 Million cell updates/sec

Title: US-09-503-089A-4  
Perfect score: 2090  
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/6CTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	99.7	411	3	US-09-236-080-6
2	2044	97.8	411	3	US-09-236-080-2
3	2044	97.8	411	3	US-09-336-643A-83
4	1855	88.8	370	3	US-09-144-914-8
5	1251.5	59.9	538	4	US-09-949-016-7001
6	1251.5	59.9	558	4	US-09-949-016-7368
7	797	38.1	393	4	US-09-432-470-2
8	797	38.1	393	4	US-09-432-470-4
9	797	38.1	419	4	US-09-949-016-6913
10	797	38.1	440	4	US-09-949-016-7809
11	551	26.4	107	3	US-09-236-080-4
12	420	20.1	499	4	US-09-561-763-2
13	420	20.1	499	4	US-09-431-367B-2
14	392	18.8	361	4	US-09-362-842-14
15	387	18.5	332	4	US-09-561-763-5
16	387	18.5	332	4	US-09-431-367B-5
17	376.5	18.0	336	3	US-08-749-816-2
18	376.5	18.0	336	3	US-09-144-914-2
19	370	17.7	394	3	US-09-144-914-4
20	345.5	16.5	388	4	US-09-949-016-7631
21	345	16.5	405	3	US-09-144-914-5
22	342	16.4	313	4	US-09-336-643A-81
23	342	16.4	313	4	US-09-561-763-8
24	342	16.4	313	4	US-09-431-367B-8
25	317.5	15.2	408	4	US-09-362-842-12
26	299.5	14.3	618	1	US-08-332-312-2
27	293	14.0	257	4	US-09-949-016-6654

28	293	14.0	273	4	US-09-949-016-7794	Sequence 7794, Ap
29	256.5	12.3	395	4	US-09-362-842-6	Sequence 6, Appli
30	219	10.4	336	1	US-08-332-313-4	Sequence 4, Appli
31	216.5	10.4	730	4	US-09-362-842-4	Sequence 4, Appli
32	216.5	10.4	741	4	US-09-362-842-67	Sequence 67, Appli
33	216.5	10.4	741	4	US-09-270-767-45442	Sequence 45442, A
34	212	10.1	401	4	US-09-561-763-11	Sequence 11, Appli
35	210.5	10.1	401	4	US-09-431-367B-11	Sequence 11, Appli
36	210.5	10.1	995	4	US-09-362-842-2	Sequence 2, Appli
37	184.5	8.8	383	3	US-08-749-816-4	Sequence 4, Appli
38	184.5	8.8	383	3	US-09-144-914-7	Sequence 7, Appli
39	172	8.2	1153	4	US-09-362-842-8	Sequence 8, Appli
40	160.5	7.7	347	3	US-08-749-816-3	Sequence 3, Appli
41	160.5	7.7	347	3	US-09-144-914-6	Sequence 6, Appli
42	152.5	7.3	197	3	US-09-336-643A-16	Sequence 16, Appli
43	141	6.7	146	4	US-09-362-842-69	Sequence 69, Appli
44	141	6.7	146	4	US-09-270-767-31685	Sequence 31685, A
45	128	6.1	988	4	US-09-614-480-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-236-080-6  
; Sequence 6, Application US/092336080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-236-080-6

Query Match 99.7%; Score 2084; DB 3; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.9e-210;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAAPDLLDPKSAQNSKPRLSPSSPTVLASRVSDSAINVMKWTSTIFLWVLYLI	60
DB	1	MAAPDLLDPKSAQNSKPRLSPSSPTVLASRVSDSAINVMKWTSTIFLWVLYLI	60
QY	61	GAAPKALEPOEISORTTIVIQOTFIAQACVNSTELDELIQIIVAAINAGIIPLGS	120
DB	61	GAAPKALEPOEISORTTIVIQOTFIAQACVNSTELDELIQIIVAAINAGIIPLGS	120
QY	121	SNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPLFGFLAGVGQ	180
DB	121	SNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPLFGFLAGVGQ	180
QY	181	LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFPALPAVIFKHIEGWSALD	240
DB	181	LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFPALPAVIFKHIEGWSALD	240
QY	241	AIYFVVTITLTITIGFDYVAGGSDIEYLFQPKVVMFTLVGLAYFAAVLSMTIGDMLRVLS	300
DB	241	AIYFVVTITLTITIGFDYVAGGSDIEYLFQPKVVMFTLVGLAYFAAVLSMTIGDMLRVLS	300
QY	301	KTKKEVGEFRAHAAEWANTVAEFKERRRSLVSIYDKFORATSVKRLKSLAELAGNHQ	360
DB	301	KTKKEVGEFRAHAAEWANTVAEFKERRRSLVSIYDKFORATSVKRLKSLAELAGNHQ	360
QY	361	ELTPCRRTLNVNHLTSERVLPLPKAESIYLNGLTPHCAGEDIAVIENMK	411
DB	361	ELTPCRRTLNVNHLTSERVLPLPKAESIYLNGLTPHCAGEDIAVIENMK	411

RESULT 2

US-09-236-080-2  
; Sequence 2, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; PRIORITY FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match 97.8%; Score 2044; DB 3; Length 411;  
Best Local Similarity 96.4%; Pred. No. 3e-206;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLI 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSTPTVLASRVSDTTINVMKWTSTIFLVVLYLI 60  
  
Qy 61 GAAVFKALEQPOEISQRTTIVIQKOTFIAQHACVNSTELDELIQIIVAAINAGIPLGNS 120  
Db 61 GATVFKALEQPEHISQRTTIVIQKOTFISQHCNVNSTELDELIQIIVAAINAGIPLGNT 120  
  
Qy 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIVALLGIFLFGFLAGVGDQ 180  
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIVALLGIFLFGFLAGVGDQ 180  
  
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
  
Qy 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300  
Db 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300  
  
Qy 301 KKTKEEVEGFRAHAEWTANVTABFKETRRRLSVIYDKFORATSVKRLSAGELAGNHQ 360  
Db 301 KKTKEEVEGFRAHAEWTANVTABFKETRRRLSVIYDKFORATSVKRLSAGELAGNHQ 360  
  
Qy 361 ELTPCRRTLNVNHLTSERVLPLLKAEISYINGLTPHCAGEDIAVIENMK 411  
Db 361 ELTPCRRTLNVNHLTSERVLPLLKAEISYINGLTPHCAGEDIAVIENIK 411

RESULT 3

US-09-336-643A-83  
; Sequence 83, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; PRIORITY FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826

; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-09-336-643A-83

Query Match 97.8%; Score 2044; DB 3; Length 411;  
Best Local Similarity 96.4%; Pred. No. 3e-206;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLI 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSTPTVLASRVSDTTINVMKWTSTIFLVVLYLI 60  
  
Qy 61 GAAVFKALEQPOEISQRTTIVIQKOTFIAQHACVNSTELDELIQIIVAAINAGIPLGNS 120  
Db 61 GATVFKALEQPEHISQRTTIVIQKOTFISQHCNVNSTELDELIQIIVAAINAGIPLGNT 120  
  
Qy 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIVALLGIFLFGFLAGVGDQ 180  
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIVALLGIFLFGFLAGVGDQ 180  
  
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240  
  
Qy 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300  
Db 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300  
  
Qy 301 KKTKEEVEGFRAHAEWTANVTABFKETRRRLSVIYDKFORATSVKRLSAGELAGNHQ 360  
Db 301 KKTKEEVEGFRAHAEWTANVTABFKETRRRLSVIYDKFORATSVKRLSAGELAGNHQ 360  
  
Qy 361 ELTPCRRTLNVNHLTSERVLPLLKAEISYINGLTPHCAGEDIAVIENMK 411  
Db 361 ELTPCRRTLNVNHLTSERVLPLLKAEISYINGLTPHCAGEDIAVIENIK 411

RESULT 4

US-09-144-914-8  
; Sequence 8, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Lazdunski, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS. THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989.6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144,914  
; EARLIER FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749,816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095,234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Murine  
; FEATURE:  
; OTHER INFORMATION: TREK-1  
US-09-144-914-8

Query Match 88.8%; Score 1855; DB 3; Length 370;

*no answer?*  
*in answer?*  
*or plug.*

Best Local Similarity 99.5%; Pred. No. 2e-186;  
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQNSKPRLSFSKPTVLAASRVESDSAINVMKWKTVSTIFLVVLYLII 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSKPTVLAASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Qy 61 GAAVFKALEQPOEISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAINAGIPLGNS 120  
Db 61 GAAVFKALEQPOEISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAINAGIPLGNS 120

Qy 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPLEGFLAGVGDO 180  
Db 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPLEGFLAGVGDO 180

Qy 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIFKHIEGSALD 240  
Db 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIFKHIEGSALD 240

Qy 241 AIYFVWITLTIGFDYVAGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300  
Db 241 AIYFVWITLTIGFDYVAGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300

Qy 301 KKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSVKSKLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSVKSKLSAELAGNHQ 360

Qy 361 ELTPCRR 368  
Db 361 ELTPCMT 368

RESULT 5  
US-09-949-016-7001  
; Sequence 7001, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7001  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7001

Query Match 59.9%; Score 1251.5; DB 4; Length 538;  
Best Local Similarity 64.3%; Pred. No. 1.1e-122;  
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

Qy 2 AAPDLLDPKSA-----AQNPKRLSFSKPTVLAASRVESDS---AINVMKWKTVSTI 50  
Db 17 AAPVCPKSNATNGQPAPAPTPTPLRSISSRATVVA-RMEGTSGQGLQTVMKWKTVAI 75

Qy 51 FLVVLYLIIGAFAVKALQPOEISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAI 110  
Db 76 FVVVVVLTGVLFRALQPOEISSQKNTIALEKAEFLRDHVCVSPQLETLIHALDAD 135

Qy 111 NAGIPLGNSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPLF 170  
Db 136 NAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCIIYAFIPLF 195

Query Match 59.9%; Score 1251.5; DB 4; Length 538;  
Best Local Similarity 64.3%; Pred. No. 1.1e-122;  
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

Qy 2 AAPDLLDPKSA-----AQNPKRLSFSKPTVLAASRVESDS---AINVMKWKTVSTI 50  
Db 17 AAPVCPKSNATNGQPAPAPTPTPLRSISSRATVVA-RMEGTSGQGLQTVMKWKTVAI 75

Qy 51 FLVVLYLIIGAFAVKALQPOEISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAI 110  
Db 76 FVVVVVLTGVLFRALQPOEISSQKNTIALEKAEFLRDHVCVSPQLETLIHALDAD 135

Qy 111 NAGIPLGNSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPLF 170  
Db 136 NAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCIIYAFIPLF 195

Qy 171 GFLLAGVGDLGTIFGKIAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIF 230  
Db 196 GFLLAGIGDQGTIFGKSIAKVEDTFIKMNVSTQKIRIISTIFILAGCIVFTVPAVIF 255

Qy 231 KHIEGSALDAIYFVVITLTITIGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289  
Db 256 KYIEGHTALESYFVVVITLTITIGFDYVAGGAGINIREWIKPLVWFWILVGLAYFAAVL 315

Qy 290 SMIGDMLRVISKKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSV--- 346  
Db 316 SMIGDMLRVLVKKTKEEVGEIKAHAAEWKANTVAEFRETRRLRSVEIHDKLQRAATIRSM 375

Qy 347 -KKLSAELAGNHQELTPCRR 369  
Db 376 ERRRLGLDQRAHSLDMLSPKRSV 399

RESULT 6  
US-09-949-016-7368  
; Sequence 7368, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7368  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7368

Query Match 59.9%; Score 1251.5; DB 4; Length 558;  
Best Local Similarity 64.3%; Pred. No. 1.2e-122;  
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

Qy 2 AAPDLLDPKSA-----AQNPKRLSFSKPTVLAASRVESDS---AINVMKWKTVSTI 50  
Db 37 AAPVCPKSNATNGQPAPAPTPTPLRSISSRATVVA-RMEGTSGQGLQTVMKWKTVAI 95

Qy 51 FLVVLYLIIGAFAVKALQPOEISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAI 110  
Db 96 FVVVVVLTGVLFRALQPOEISSQKNTIALEKAEFLRDHVCVSPQLETLIHALDAD 155

Qy 111 NAGIPLGNSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPLF 170  
Db 156 NAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCIIYAFIPLF 215

Qy 171 GFLLAGVGDLGTIFGKIAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIF 230  
Db 216 GFLLAGIGDQGTIFGKSIAKVEDTFIKMNVSTQKIRIISTIFILAGCIVFTVPAVIF 275

Qy 231 KHIEGSALDAIYFVVITLTITIGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289  
Db 276 KYIEGHTALESYFVVVITLTITIGFDYVAGGAGINIREWIKPLVWFWILVGLAYFAAVL 335

Qy 290 SMIGDMLRVISKKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSV--- 346  
Db 336 SMIGDMLRVLVKKTKEEVGEIKAHAAEWKANTVAEFRETRRLRSVEIHDKLQRAATIRSM 395

Qy 347 -KKLSAELAGNHQELTPCRR 369  
Db 396 ERRRLGLDQRAHSLDMLSPKRSV 419

RESULT 7  
US-09-432-470-2  
; Sequence 2, Application US/09432470  
; Patent No. 6426197  
; GENERAL INFORMATION:  
; APPLICANT: David Malcolm Duckworth  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30190  
; CURRENT APPLICATION NUMBER: US/09/432,470  
; EARLIER APPLICATION NUMBER: UK 9923668.9  
; EARLIER FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: UK 9824048.4  
; EARLIER FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-432-470-2

Query Match 38.1%; Score 797; DB 4; Length 393;  
Best Local Similarity 51.1%; Pred. No. 4.5e-75;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
QY 42 MKWKTSTIFLVVLYLIIGAAVFKALQPOEISORTTIVIOKQTFIAQHACVNSTELDE 101  
Db 1 MRSTTLALLALVLYLVSGALVFRALQPEHQQAQRELGEVREKFLRAHPCVSDQELGL 60  
QY 102 LIQQIVAAINAGIIPLGSSNOVSH--WDLGSSPFFAGTIVITIGFNGISPRTEGGKIFC 159  
Db 61 LIKEVADALGGADPETNSTSSSHSAMDLSGSAFFSGTITITIGYGNVALRTDAGRLFC 120  
QY 160 IYALLGIPFLGFLAGVDQGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFC 219  
Db 121 IFYALVGIPFLGILLAGVDRGLSSLRHGIGHIEAIFLKHVPPPELVRLVLSAMFLLLG 180  
QY 220 VLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279  
Db 181 LLFVLTPTTFVFCYMEDWSKLEAIFYVITLTITIGFDYVAGADPRQDSPAYQPLVWFIL 240  
QY 280 VGLAYFAAVLSMIGDNLRVISKKEEVEGFRAHAAEWNTANVTA 323  
Db 241 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 284

RESULT 8  
US-09-432-470-4  
; Sequence 4, Application US/09432470  
; Patent No. 6426197  
; GENERAL INFORMATION:  
; APPLICANT: David Malcolm Duckworth  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30190  
; CURRENT APPLICATION NUMBER: US/09/432,470  
; EARLIER APPLICATION NUMBER: UK 9923668.9  
; EARLIER FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: UK 9824048.4  
; EARLIER FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-432-470-4

Query Match 38.1%; Score 797; DB 4; Length 393;  
Best Local Similarity 51.1%; Pred. No. 4.5e-75;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
QY 42 MKWKTSTIFLVVLYLIIGAAVFKALQPOEISORTTIVIOKQTFIAQHACVNSTELDE 101  
Db 1 MRSTTLALLALVLYLVSGALVFRALQPEHQQAQRELGEVREKFLRAHPCVSDQELGL 60  
QY 102 LIQQIVAAINAGIIPLGSSNOVSH--WDLGSSPFFAGTIVITIGFNGISPRTEGGKIFC 159  
Db 61 LIKEVADALGGADPETNSTSSSHSAMDLSGSAFFSGTITITIGYGNVALRTDAGRLFC 120  
QY 160 IYALLGIPFLGFLAGVDQGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFC 219  
Db 121 IFYALVGIPFLGILLAGVDRGLSSLRHGIGHIEAIFLKHVPPPELVRLVLSAMFLLLG 180  
QY 220 VLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279  
Db 181 LLFVLTPTTFVFCYMEDWSKLEAIFYVITLTITIGFDYVAGADPRQDSPAYQPLVWFIL 240  
QY 280 VGLAYFAAVLSMIGDNLRVISKKEEVEGFRAHAAEWNTANVTA 323  
Db 241 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 284

RESULT 9  
US-09-949-016-6913  
; Sequence 6913, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6913  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6913

Query Match 38.1%; Score 797; DB 4; Length 419;  
Best Local Similarity 51.1%; Pred. No. 4.9e-75;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
QY 42 MKWKTSTIFLVVLYLIIGAAVFKALQPOEISORTTIVIOKQTFIAQHACVNSTELDE 101  
Db 27 MRSTTLALLALVLYLVSGALVFRALQPEHQQAQRELGEVREKFLRAHPCVSDQELGL 86  
QY 102 LIQQIVAAINAGIIPLGSSNOVSH--WDLGSSPFFAGTIVITIGFNGISPRTEGGKIFC 159  
Db 87 LIKEVADALGGADPETNSTSSSHSAMDLSGSAFFSGTITITIGYGNVALRTDAGRLFC 146  
QY 160 IYALLGIPFLGFLAGVDQGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFC 219  
Db 147 IFYALVGIPFLGILLAGVDRGLSSLRHGIGHIEAIFLKHVPPPELVRLVLSAMFLLLG 206  
QY 220 VLFVALPAVIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279  
Db 207 LLFVLTPTTFVFCYMEDWSKLEAIFYVITLTITIGFDYVAGADPRQDSPAYQPLVWFIL 266  
QY 280 VGLAYFAAVLSMIGDNLRVISKKEEVEGFRAHAAEWNTANVTA 323  
Db 267 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 310



RESULT 10  
US-09-949-016-7809  
; Sequence 7809, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7809  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7809

Query Match 38.1%; Score 797; DB 4; Length 440;  
Best Local Similarity 51.1%; Pred. No. 5.3e-75;  
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;  
QY 42 MKWTKVSTFLVVLVLIIGAAVFKALEQEQEISQRTTIVIQKOTFIAQHACVNSTELDE 101  
DB MRSTLLALLLVLYVSGALVFPALQEPHQQAQRELGVEVREKFLRAHPCVSQELGL 107  
QY 102 LIQQTVAINAGIIPLGSSNOVSH--WDLGSSFFAGTIVTTIGFNGISPRTEGKIFC 159  
DB 108 LIKEVADALGGADPETNSTSSSHAWDLGSAFFPGSTIITIGYGNVALRTDAGRLFC 167  
QY 160 IYALLGLPFLGFLAGVDGLTIFGKIAKVEDTFIKWVSOQTKIRIISTIFILFGC 219  
DB 168 IFYALVGLPFLGILLAGVDRGSSLRHGIGHIEAIFLKHVPPBLRVLSAWLFLG 227  
QY 220 VLFVALPAVIFKHIEGWSALDAIYFVWITLTITIGFDYVAGSDIEYLDYFKVPVWFIL 279  
DB 228 LLFVLTPFVFCYMEDWSKLEAIYFVITVITVGVGDYVAGADPRQDSPAYQPLWFWIL 287  
QY 280 VGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAVTA 323  
DB 288 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 331

RESULT 11  
US-09-236-080-4  
; Sequence 4, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-236-080-4

Query Match 26.4%; Score 551; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.7e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 119 NSSQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLFGV 178  
DB 1 NSSQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLFGV 60  
QY 179 DQLGTIFGKIAKVEDTFIKWVSOQTKIRIISTIFILFGCVLFVAL 225  
DB 61 DQLGTIFGKIAKVEDTFIKWVSOQTKIRIISTIFILFGCVLFVAL 107

RESULT 12  
US-09-561-763-2  
; Sequence 2, Application US/09561763  
; Patent No. 6664373  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; CURRENT FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999  
; PRIOR APPLICATION NUMBER: US 09/259,951  
; PRIOR FILING DATE: 01-03-1999  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-763-2

Query Match 20.1%; Score 420; DB 4; Length 499;  
Best Local Similarity 30.8%; Pred. No. 3e-35;  
Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11;  
QY 54 VVLYLIIGAAVFKALEQEQEISQRTTIVIQKOTFIAQHACVNSTELDELIQOIVAAINAG 113  
DB 12 IIFVLAIGAAIFVELEBPHWEAKQVYTKLHLLKBPCLGQEGDLKILEVVSDAAGQ 71  
QY 114 IIPGNSNVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLFGV 173  
DB 72 VAITGNQT--FNNWNWPNAMIFAAATVITIGYGNVAPKTPAGRLFCVYGLFGVPL--C 126  
QY 174 LAGVGDQGTIFGKIAKVEDTFIKWVSOQTKIRIISTIFILFGCVLFVALPAVIEKHI 233  
DB 127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFVGVVHLVLPFVFWMT 185  
QY 234 EGWSALDAIYFVWITLTITIGFDYVAG--GSDIEYLDYFKVPVWFVWILVGLAYFAAVLSMI 292  
DB 186 EGMVIEGLYYSFITISTIGFDYVAGVWNPVSNYHALYRYFVLMVILGLAW---LSLF 241  
QY 293 GDWLRVSKTKKEVGEFRAHAAEWNTAVTAETRRRLSVEIYDKFORATSVGRKLSA 352  
DB 242 VNW-----KVSMP-----VEVHKAIKRRRR-----RKESF 267  
QY 353 ELAGNHQELTPCRRTLNVNHLTSEV--LPPLLKAESIY 391  
DB 268 E-SSPHS-----RRALQVKGSTASKOVNIPFSLSKKEEY 301

RESULT 13  
US-09-431-367B-2  
; Sequence 2, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP  
; CURRENT APPLICATION NUMBER: US/09/431,367B  
; CURRENT FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/259,951

```
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-2

Query Match      20.1%; Score 420; DB 4; Length 499;
Best Local Similarity 30.8%; Pred. No. 3e-35;
Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11;

Qy 54 VVLYLIIGAAVFKALEQPOEISQRTTIVIQOTFIAQHACVNSTELDELIIQIIVAANAG 113
Db 12 IIFYLGAALFEVLEEPHWEAKKNYTKLHLLKEPFCGQGLQKILEVWSDAAGQG 71

Qy 114 IIPLGSSNOVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIPFGFL 173
Db 72 VAITGNQT--FNNWNPNAIFAATVITIGYGNVAPKTPAGRLFCVYGLFGVPL--C 126

Qy 174 LAGVGDQLTGIFGKIAKVETFTKWNVSQTKIRIISTIIIFILGCVLFVALPAVIFKHI 233
Db 127 LTWI-SALGKFPFGRAKRLGQLTKRGVSLRKAQITCTVIFIVWGLVHLVIPPVFMVT 185

Qy 234 EGWSALDAIFYVWLTITIGFDYVAG-GSDIEYLDVKVPVWFWILVGLAYFAAVLSMI 292
Db 186 EGMWYIEGLYFISFITISTIGFGDFVAGVNPNSANTHALYRYFVELWYIYGLAW----LSLP 241

Qy 293 GDLRLVISKTKKEEVGFRAHAEBWNTANVTAEFKTRRRLSVEIYDKFQRATSVKRLSA 352
Db 242 VNW-----KVSMP-----VEVHKAIKRRER-----RKESF 267

Qy 353 ELAGNHQELTPCRRITVSNHLTSEREV--LPPLLKASIIY 391
Db 268 E-SSPHS-----RKALQVGKSTASKDVNIFSLSKKEEY 301

RESULT 14
US-09-362-842-14
; Sequence 14, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIX
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Leptinotarsa decemlineata
US-09-362-842-14

Query Match      18.8%; Score 392; DB 4; Length 361;
Best Local Similarity 35.6%; Pred. No. 1.6e-32;
Matches 89; Conservative 53; Mismatches 86; Indels 22; Gaps 6;

Qy 56 LYLIIGAAVFKALEQPOEISQRTTIVIQOTFIAQHACVNSTELDELIIQIIVAANAGII 115
Db 55 MFLCSGAAVFSYFEAPEERALARVLGTAVQKFLVSNPNVTADLEELIVEIVRANRGVS 114

Qy 116 PLGNSSNOVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIPFGFLA 175
Db 115 AIENATSE-PNWSFGQSFFASTVITIGYGHVPLSNKGLFCMFTAVAGIPLTVLLS 173

Qy 176 GVGDQL--GTIFGKIAKVETFTKWNVSQ-----TKIRIISTIIIFILGCVLFVALP 226
Db 176 GVGDQL--GTIFGKIAKVETFTKWNVSQ-----TKIRIISTIIIFILGCVLFVALP 226

; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-5

Query Match      18.5%; Score 387; DB 4; Length 332;
Best Local Similarity 35.5%; Pred. No. 4.8e-32;
Matches 88; Conservative 51; Mismatches 95; Indels 14; Gaps 6;

Qy 50 IFLVVLYLIIGAAVFKALEQPOEISQRTTIVIQOTFIAQHACVNSTELDELIIQIIVAA 109
Db 25 LLLAYLAYLALGTGVFWTLEGRAAQSSRSFQDKWELLQNFCLDRPALDSLIRDVVQA 84

Qy 110 INAGIIPLGSSNOVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIP 169
Db 85 YKNGASLSNNTS-MGRWELVGSFFSVSTITTIGYGNLSNPNMTMAARLFCIFFALVGIPL 143

Qy 170 FGELLAGVGDLGTIFGKGI-----AKVEDTFKWNVSQTKIRIISTIIIFILGCVLFVAL 225
Db 144 NLVVL-----NRLGHLMOQGYNNHNASRLGGT---WQ-DPDKARWLAGSGALLSLLLFL 195

Qy 226 PAVIFKHIEGWSALDAIFYVWLTITIGFDYVAGGSDIE-YLDFYKPVVWFWILVGLAY 284
Db 196 PPLLFSHMEGWSYTEGYFAFILTSTVGFDYVIGMNPQSRYPLWYKXNWSLSLWILFGWAW 255

Qy 285 FAAVLSMI 292
Db 256 LALIILKI 263

Search completed: July 13, 2005, 08:47:05
Job time : 27.3635 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model.

Run on: July 13, 2005, 07:58:54 ; Search time 101.398 Seconds  
(without alignments)  
1567.669 Million cell updates/sec

Title: US-09-503-089A-2  
Perfect score: 2100  
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNLTPHCAGEIAVIENTIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2100	100.0	411	3 AAE10341	Aae10341 Human TRE
2	2095	99.8	411	2 AAY34133	Aay34133 Human pot
3	2095	99.8	411	2 AAY28496	Aay28496 h-TREK1 p
4	2095	99.8	411	4 AAB50044	Aab50044 Human TRE
5	2095	99.8	411	7 ADP03586	Adp03586 Human GPC
6	2095	99.8	411	8 ADQ76698	Adq76698 Human two
7	2092	99.6	411	5 AAE16597	Aae16597 Human TWI
8	2089	99.5	422	7 ADP03575	Adp03575 Human GPC
9	2062	98.2	426	4 AAU07618	Aau07618 Human pot
10	2058	98.0	426	4 AAU07622	Aau07622 Human pot
11	2057	98.0	426	4 AAU07623	Aau07623 Human pot
12	2054	97.8	426	4 AAU07625	Aau07625 Human pot
13	2053	97.8	426	4 AAU07624	Aau07624 Human pot
14	2041	97.2	411	3 AAE10342	Aae10342 Murine TR
15	2035	96.9	411	2 AAY28497	Aay28497 Mouse h-T
16	1833	87.3	370	2 AAY30648	Aay30648 A mechani
17	1638.5	78.0	337	6 ABR41487	Abr41487 Human DIT
18	1243	59.2	538	5 AAB47930	Aab47930 Human TRE
19	1243	59.2	538	5 AAE16596	Aae16596 Human TWI
20	1243	59.2	538	5 ABP69333	Abp69333 Human pol
21	1243	59.2	543	5 AAE21804	Aae21804 Human TRE
22	1243	59.2	543	5 AAU81354	Aau81354 Human hum
23	1243	59.2	543	5 AAU79472	Aau79472 Human nov
24	1243	59.2	543	5 ABB83542	Abb83542 Hypothala
25	1243	59.2	543	6 ADA05746	Ada05746 Human NOV

26	1243	59.2	543	7 ADE08315	Ade08315 Novel pro
27	1243	59.2	543	8 ADN62910	Adn62910 Human NOV
28	1239	59.0	543	5 AAU79473	Aau79473 Human nov
29	1215.5	57.9	724	5 AAO14193	Aao14193 Human tra
30	988	47.0	228	8 ADJ27190	Adj27190 Human TRI
31	803	38.2	392	6 ABU60891	Abu60891 Human G p
32	803	38.2	393	3 AAY94426	Aay94426 Human h-T
33	803	38.2	393	3 AAY94425	Aay94425 Human h-T
34	803	38.2	393	4 AAG67777	Aag67777 Human mec
35	803	38.2	419	5 AAG78406	Aag78406 Amino aci
36	803	38.2	419	7 AAE38597	Aae38597 Human pot
37	803	38.2	419	7 ADK52550	Adk52550 Hematolog
38	803	38.2	419	8 ADH51639	Adh51639 Human 123
39	803	38.2	419	8 ADI27936	Adi27936 Human TWI
40	803	38.2	419	8 ADR44894	Adr44894 Polypepti
41	803	38.2	1314	4 AAU04571	Aau04571 Human G-p
42	803	38.2	1314	6 ABU60872	Abu60872 Human G p
43	776.5	37.0	398	2 AAY30647	Aay30647 A mechani
44	768.5	36.6	398	5 AAE16598	Aae16598 Human TWI
45	636	30.3	383	4 ABG02731	Abg02731 Novel hum

## ALIGNMENTS

RESULT 1  
AAE10341  
ID AAE10341 standard; protein; 411 AA.  
XX  
AC AAE10341;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Human TREK-1 potassium channel protein.  
XX  
KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;  
KW amnesia.  
XX  
OS Homo sapiens.  
XX  
PN WO200047738-A2.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-IB000226.  
XX  
PR 12-FEB-1999; 99US-0119727P.  
PR 11-FEB-2000; 2000US-00503089.  
(CNRS ) CNRS CENT NAT RECH SCI.  
Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
XX  
WPI; 2000-549146/50.  
DR N-PSDB; AAD17496.  
XX  
PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
transfecting cells to be used to identify compounds with anesthetic  
properties.  
XX  
Claim 3; Page 28; 39pp; English.  
XX  
The invention relates to human and mouse TREK-1 potassium channel  
proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
useful for transfecting cells to induce expression of the TREK-1  
potassium channel protein. These cells are then used in assays to  
identify compounds which have anaesthetic properties, producing a safe,  
reversible state of unconsciousness with concurrent amnesia and analgesia  
in a mammal upon inhalation. The present sequence is human TREK-1  
potassium channel protein  
XX  
Sequence 411 AA;

Query Match 100.0%; Score 2100; DB 3; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-210;  
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIFLVVLYLII 60  
 |||||  
 DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIFLVVLYLII 60  
 |||||

QY 61 GATVFKALEQPHSEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120  
 |||||  
 DB 61 GATVFKALEQPHSEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120  
 |||||

QY 121 SNOISHWDLGSSFFPAGTVITIGFGNISPRTGGKIFCIIVALLGIPFLFGFLLAGVGQ 180  
 |||||  
 DB 121 SNOISHWDLGSSFFPAGTVITIGFGNISPRTGGKIFCIIVALLGIPFLFGFLLAGVGQ 180  
 |||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240  
 |||||  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240  
 |||||

QY 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 DB 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIRKRLSIAELAGNHQ 360  
 |||||  
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIRKRLSIAELAGNHQ 360  
 |||||

QY 361 ELTPCRRTLTSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411  
 |||||  
 DB 361 ELTPCRRTLTSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411  
 |||||

RESULT 2  
 AAY34133  
 ID AAY34133 standard; protein; 411 AA.  
 XX AAY34133;  
 XX 30-NOV-1999 (first entry)  
 XX Human potassium channel K-Hnov59.  
 XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
 XX cardiovascular disorder; CNS disorder; renal disorder.

OS Homo sapiens.  
 XX WO9943696-A1.  
 XX 02-SEP-1999.  
 XX 22-FEB-1999; 99WO-US003826.  
 XX 25-FEB-1998; 98US-0076687P.  
 XX 07-AUG-1998; 98US-0095836P.  
 XX 19-JAN-1999; 99US-0116448P.  
 XX (AXYS-) AXYS PHARM INC.  
 XX Miller AP, Curran ME, Hu P, Rutter M, Wang J;  
 XX WPI; 1999-527591/44.  
 XX N-PSDB; AA211915.  
 XX New nucleic acids encoding mammalian K-Hnov potassium channel proteins,  
 XX useful for the diagnosis and treatment of episodic ataxia with myokymia,  
 XX cardiac arrhythmia, epilepsy and Bartter's syndrome.  
 XX Claim 3; Page 104-105; 112pp; English.  
 XX This sequence represents the human K-Hnov59 potassium channel. K-Hnov  
 XX proteins have a high degree of homology to known potassium channels and

CC may be alpha subunits, which form the functional channel, or accessory  
 CC subunits that act to modulate the channel activity. K-Hnov59 is a 4  
 CC transmembrane domain, 2 pore domain potassium channel. The gene is  
 CC located on chromosome 19, determined via PCR chromosomal localisation  
 CC using primers AA211939 and AA211940. K-Hnov cDNAs were isolated by  
 CC extension of expressed sequence tags (ESTs) which were related but not  
 CC identical to known human potassium channels. Potential polymorphisms  
 CC detected as sequence variants between multiple independent clones.  
 CC Potassium channels have critical roles in various cell types and  
 CC biochemical pathways. Defective potassium channels are known to cause  
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia  
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium  
 CC channels are critical components of virtually all cells, it is likely  
 CC that abnormal potassium channels are also implicated in certain renal,  
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides  
 CC encoding K-Hnov proteins may be used for identifying homologous or  
 CC related proteins and the DNA sequences encoding them. They may be used to  
 CC produce compositions that modulate the expression and function of the  
 CC K-Hnov protein and in studying the biochemical pathways associated with  
 CC it. They may also be used for the recombinant production of K-Hnov  
 CC protein in fermentation cultures. Additionally, such nucleotides may be  
 CC used in gene therapy protocols for the treatment of diseases associated  
 CC with abnormal potassium channels  
 XX

SQ Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 2; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIFLVVLYLII 60  
 |||||  
 DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIFLVVLYLII 60  
 |||||

QY 61 GATVFKALEQPHSEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120  
 |||||  
 DB 61 GATVFKALEQPHSEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120  
 |||||

QY 121 SNOISHWDLGSSFFPAGTVITIGFGNISPRTGGKIFCIIVALLGIPFLFGFLLAGVGQ 180  
 |||||  
 DB 121 SNOISHWDLGSSFFPAGTVITIGFGNISPRTGGKIFCIIVALLGIPFLFGFLLAGVGQ 180  
 |||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240  
 |||||  
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240  
 |||||

QY 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 DB 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIRKRLSIAELAGNHQ 360  
 |||||  
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIRKRLSIAELAGNHQ 360  
 |||||

QY 361 ELTPCRRTLTSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411  
 |||||  
 DB 361 ELTPCRRTLTSVNLHTSERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411  
 |||||

RESULT 3  
 AAY28496  
 ID AAY28496 standard; protein; 411 AA.  
 XX AAY28496;  
 XX 12-OCT-1999 (first entry)  
 XX h-TREK1 polypeptide.  
 XX h-TREK1; two pore potassium channel; inflammatory disease;  
 XX chromosome 1q32.  
 XX Homo sapiens.

XX WO9937762-A1.  
 XX  
 XX  
 XX 29-JUL-1999.  
 XX  
 XX 02-DEC-1998; 98WO-EP007805.  
 XX  
 XX 27-JAN-1998; 98EP-00300570.  
 XX 09-OCT-1998; 98GB-00022135.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Meadows HJ, Chapman CG;  
 XX  
 XX WPI; 1999-469126/39.  
 XX N-PSDB; AA2000039.  
 XX  
 XX New two pore potassium channel used for, e.g. treatment of cancer,  
 XX pulmonary, cardiovascular and inflammatory diseases.  
 XX  
 XX Claim 3; Page 24; 44pp; English.  
 XX  
 XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1  
 XX polynucleotide AA2000039. h-TREK1 is a two pore potassium channel, and the  
 XX gene maps to human chromosome 1q32, between the markers D15237 and  
 XX W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
 XX disease or susceptibility to a disease related to expression or activity  
 XX of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 XX treatment of diseases including cancer, pulmonary, cardiovascular, and  
 XX inflammatory diseases, pain, psychiatric disorders including depression  
 XX and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 XX stroke, and head trauma and neurological disorders including migraine  
 XX  
 XX Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 2; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60  
 Db 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60  
 QY 61 GATVFKALEOPHEISQRTTIVIQKTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120  
 Db 61 GATVFKALEOPHEISQRTTIVIQKTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120  
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 Db 121 SNOISHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240  
 Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240  
 QY 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300  
 Db 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300  
 QY 301 KTKKEVGFRAHAAEWNTVAEFKTRRRRLSVEIYDKFORATSKRKLSELAGNHNQ 360  
 Db 301 KTKKEVGFRAHAAEWNTVAEFKTRRRRLSVEIYDKFORATSKRKLSELAGNHNQ 360  
 QY 361 ELTPCRRTLISVNLHTSERDVLPLLLATSTIYLNGLTPHCAGEIAVNIENK 411  
 Db 361 ELTPCRRTLISVNLHTSERDVLPLLLATSTIYLNGLTPHCAGEIAVNIENK 411

RESULT 4  
 AAB50044  
 ID AAB50044 standard; protein; 411 AA.  
 XX  
 AC AAB50044;

XX 19-MAR-2001 (first entry)  
 XX  
 XX Human TREK.  
 XX  
 XX Human; TREK; 2P domain potassium channel; resting membrane potential;  
 XX neuronal excitability; neurotransmitter release modulation; epilepsy;  
 XX neurological disorder; sleep-related disorder; cognitive dysfunction;  
 XX attention deficit disorder; addiction; anxiety; phobia;  
 XX Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
 XX erectile dysfunction; alopecia.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2000072863-A2.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 01-JUN-2000; 2000WO-GB0002107.  
 XX  
 XX 01-JUN-1999; 99GB-00012733.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Hervieu GJ, Meadows HJ, Randall AD;  
 XX  
 XX WPI; 2001-080422/09.  
 XX N-PSDB; AAC90412.  
 XX  
 XX Use of human TREK1 polypeptide, polynucleotides encoding them and  
 XX modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
 XX disorders, addiction and dyskinesias including Parkinson's and  
 XX Huntington's chorea.  
 XX  
 XX Claim 7; Page 29; 35pp; English.

The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
 2P domain potassium channel family of proteins which play a part in the  
 control of resting membrane potential. Modulation of these channels will  
 therefore affect neuronal excitability, thereby leading to a modulation  
 of neurotransmitter release and activity of neuronal networks. Such  
 modulation therefore may be useful for the treatment of certain  
 neurological conditions such as epilepsy, sleep-related disorders,  
 cognitive dysfunction, attention deficit disorder, addiction,  
 anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
 incontinence, erectile dysfunction or alopecia

Query Match 99.8%; Score 2095; DB 4; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60  
 Db 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60  
 QY 61 GATVFKALEOPHEISQRTTIVIQKTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120  
 Db 61 GATVFKALEOPHEISQRTTIVIQKTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120  
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 Db 121 SNOISHWDLGSSFFAGTIVTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ 180  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240  
 Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240  
 QY 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300  
 Db 241 AIYFVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEVGEFRAHAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360  
 |||||  
 Db 301 KKTKEVGEFRAHAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360  
 |||||  
 QY 361 ELTPCRRRLTSVNNHLTNERDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411  
 |||||  
 Db 361 ELTPCRRRLTSVNNHLTNERDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411  
 |||||

## RESULT 5

ADP03586

ID ADP03586 standard; protein; 411 AA.

XX AC ADP03586;

XX DT 29-JUL-2004 (first entry)

XX DE Human GPCR potassium channel, subfamily K, member 2 protein.

XX KW GPCR, G-protein coupled receptor; neuroprotective; nootropic;  
 KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;  
 KW anticonvulsant; antiparkinsonian; cytotstatic; cardiac; hypotensive;  
 KW antianalgesic; anorectic; anti-HIV; antiaesthatic; osteopathic;  
 KW uropathic; antitumor; antiallergic; cell cycle regulation; neurological;  
 KW severe mental retardation; dyskinesia; brain; spinal cord; affective;  
 KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;  
 KW eating; HIV infection; cancer; metabolic; pituitary;  
 KW chromosome identification; gene therapy; human; receptor;  
 KW potassium channel subfamily K member 2.

XX OS Homo sapiens.

XX PN WO2003062393-A2.

XX PD 31-JUL-2003.

XX PF 22-JAN-2003; 2003WO-US001911.

XX PR 22-JAN-2002; 2002US-0350724P.

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Ramanathan CS, Gopal S, Mintier G, Feder JN;

XX DR WPI; 2003-618283/58.

XX PT New nucleic acid molecule encoding a human G-protein coupled receptor,  
 useful for diagnosing, preventing or treating diseases involving the  
 PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or  
 PT cancer.

XX PS Example 1; SEQ ID NO 31; 224pp; English.

XX CC The invention relates to a novel isolated GPCR (G-protein coupled  
 CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
 CC the invention demonstrate neuroprotective, nootropic, tranquiliser,  
 CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,  
 CC antiparkinsonian, cytotstatic, cardiac, hypotensive, antianalgesic,  
 CC analgesic, anorectic, anti-HIV, antiaesthatic, osteopathic, uropathic,  
 CC antitumor and antiallergic properties. The nucleic acid molecule and  
 CC polypeptide of the invention may be useful in diagnosing, preventing,  
 CC treating or ameliorating a medical condition, such as a disorder related  
 CC to aberrant G-protein coupled signalling, a disorder related to aberrant  
 CC cell cycle regulation, neurological disorders, severe mental retardation  
 CC and dyskinesias, brain disorders, spinal cord disorders, affective  
 CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
 CC disorders, immune-related disorders, endocrinal diseases, growth  
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
 CC chromosome identification, in identifying organisms from minute  
 CC biological samples, in gene therapy or as a molecular weight marker. The  
 CC current sequence is that of a human GPCR (G-protein coupled receptor)  
 CC protein of the invention which was used for homology purposes.

XX SQ Sequence 411 AA;  
 Query Match 99.8%; Score 2095; DB 7; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII 60  
 |||||  
 Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII 60  
 |||||  
 QY 61 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNVSTELDELIQIIVAAINAGIIPLGNT 120  
 |||||  
 Db 61 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNVSTELDELIQIIVAAINAGIIPLGNT 120  
 |||||  
 QY 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIFLFGELLAGVGDO 180  
 |||||  
 Db 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIFLFGELLAGVGDO 180  
 |||||  
 QY 181 LGTIFGKGIKVEDDFIKWVNSQTKIRIISTIFLFGCVLFVALPAIFKHIEGWSALD 240  
 |||||  
 Db 181 LGTIFGKGIKVEDDFIKWVNSQTKIRIISTIFLFGCVLFVALPAIFKHIEGWSALD 240  
 |||||  
 QY 241 AIYFVVIITLTITIGFGDYVAGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 Db 241 AIYFVVIITLTITIGFGDYVAGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300  
 |||||  
 QY 301 KKTKEVGEFRAHAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360  
 |||||  
 Db 301 KKTKEVGEFRAHAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360  
 |||||  
 QY 361 ELTPCRRRLTSVNNHLTNERDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411  
 |||||  
 Db 361 ELTPCRRRLTSVNNHLTNERDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411  
 |||||

## RESULT 6

ADQ76698

ID ADQ76698 standard; protein; 411 AA.

XX AC ADQ76698;

XX DT 07-OCT-2004 (first entry)

XX DE Human two pore domain potassium channel TREK-1.

XX KW TREK-1; sleep; two pore domain potassium channel; sedative; hypnotic;  
 XX human.

XX OS Homo sapiens.

XX PN WO2004058325-A2.

XX PD 15-JUL-2004.

XX PF 23-DEC-2003; 2003WO-US040913.

XX PR 23-DEC-2002; 2002US-0436201P.

XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.

XX PI Tononi G, Cirelli C;

XX DR WPI; 2004-534024/51.

XX PD GENBANK; NM014217.

XX PT Identifying a Drosophila mutant fly with a no rebound, short sleep and/or  
 PT no sleep deprivation resistant phenotype, for identifying sleep-related  
 PT molecular targets, comprises recording sleep quantity of the mutant fly.

XX PS Claim 12; SEQ ID NO 2; 83pp; English.

XX CC The present sequence is that of the human two pore domain K+ channel TREK

CC -1. In rats, TREK-1 is highly expressed in much of the brain and is  
 CC inhibited by protein kinase C and protein kinase C mediated  
 CC phosphorylation. It is activated by volatile general anaesthetics and is  
 CC expressed at high levels in the brain of sleep animals. Based on these  
 CC criteria and on experimental results, it is hypothesized that TREK-1 is a  
 CC key mediator of sleep (when open) and waking (when closed). The invention  
 CC provides methods for identifying a sleep- or wakefulness-promoting  
 CC compound based on the compound's ability to modulate two pore domain K+  
 CC channels such as TREK-1. It also provides screening methods for isolating  
 CC short sleep, no rebound and sleep deprivation resistant Drosophila  
 CC mutants useful for identifying sleep-related molecular targets.

XX Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 8; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;  
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GATVFKALEOPHEISORTTIVIQKTFISQHSVCNSTELDELIIQIIVAAINAGIPLGNT 120

DB 61 GATVFKALEOPHEISORTTIVIQKTFISQHSVCNSTELDELIIQIIVAAINAGIPLGNT 120

QY 121 SNOIASHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

DB 121 SNOIASHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIPFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIPFKHIEGWSALD 240

QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

DB 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

QY 361 ELTPCRRTLTSVNLHTNEDVLPPLKTESIYLNGLTPHCAGEBIAVNIK 411

DB 361 ELTPCRRTLTSVNLHTNEDVLPPLKTESIYLNGLTPHCAGEBIAVNIK 411

RESULT 7

AAE16597

ID AAE16597 standard; protein; 411 AA.

AC AAE16597;

XX 18-APR-2002 (first entry)

XX Human TWIK-Related K+ Channel-1 (TREK-1) protein.

XX Human TWIK-Related K+ Channel-1 (TREK-1) protein.

XX Human; TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 47..65

FT /note="M1 membrane spanning segment"

FT Domain 127..150

FT /note="P1 pore domain"

FT Region 158..178

FT /note="M2 membrane spanning segment"

FT Region 209..230

FT /note="M3 membrane spanning segment"

FT Domain 236..259

FT /note="P2 pore domain"

FT Region 274..293

FT /note="M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX New mammalian K+ channel protein with two pore domains, for screening

XX various compounds, particularly for identifying biologically active

XX compounds with anaesthetic properties.

XX Disclosure; Fig 1A; 50pp; English.

XX The invention relates to a mammalian K+ channel protein with two pore

XX domains, called TREK2 (TWIK-Related K+ Channel). The protein produces

XX currents whose current-voltage relationship is slightly inwardly

XX rectifying in high symmetrical K+ conditions. TREK2 is a member of the

XX fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene

XX located on chromosome 14q31 is abundantly expressed in kidney, pancreas

XX and moderately in testis, brain, colon and small intestine. The mammalian

XX K+ channel protein is useful in methods for screening various compounds.

XX In particular, the protein is useful in methods for identifying

XX biologically active compounds with anaesthetic properties. The present

XX sequence is TREK-1 protein used in the invention

XX Sequence 411 AA;

XX Query Match 99.6%; Score 2092; DB 5; Length 411;

XX Best Local Similarity 99.8%; Pred. No. 6e-209;

XX Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GATVFKALEOPHEISORTTIVIQKTFISQHSVCNSTELDELIIQIIVAAINAGIPLGNT 120

DB 61 GATVFKALEOPHEISORTTIVIQKTFISQHSVCNSTELDELIIQIIVAAINAGIPLGNT 120

QY 121 SNOIASHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

DB 121 SNOIASHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIPFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIPFKHIEGWSALD 240

QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

DB 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

QY 361 ELTPCRRTLTSVNLHTNEDVLPPLKTESIYLNGLTPHCAGEBIAVNIK 411

DB 361 ELTPCRRTLTSVNLHTNEDVLPPLKTESIYLNGLTPHCAGEBIAVNIK 411

RESULT 8

ADP03575

ID ADP03575 standard; protein; 422 AA.

XX ADP03575;  
AC  
XX  
DT 29-JUL-2004 (first entry)  
DE  
XX  
DE Human GPCR twin pore channel" protein variant "Gene 9" protein.  
XX  
XX GPCR; G-protein coupled receptor; neuroprotective; nootropic;  
KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;  
KW anticonvulsant; antiparkinsonian; cytotstatic; cardiant; hypotensive;  
KW antitanginal; analgesic; anorectic; anti-HIV; antiaethmatic; osteopathic;  
KW uropathic; antituler; antiallergic; cell cycle regulation; neurological;  
KW severe mental retardation; dyskinesia; brain; spinal cord; affective;  
KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;  
KW eating; HIV infection; cancer; metabolic; pituitary;  
KW chromosome identification; gene therapy; human; receptor;  
KW twin pore channel; potassium channel subfamily K member 2 variant.  
XX  
XX Homo sapiens.  
XX WO2003062393-A2.  
XX  
XX 31-JUL-2003.  
XX  
XX 22-JAN-2003; 2003WO-US001911.  
XX  
XX 22-JAN-2002; 2002US-0350724P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Ramanathan CS, Gopal S, Mintier G, Feder JN;  
XX  
XX WPI; 2003-618283/58.  
DR N-PSDB; ADP03564.  
XX  
XX New nucleic acid molecule encoding a human G-protein coupled receptor,  
PT useful for diagnosing, preventing or treating diseases involving the  
PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or  
PT cancer.  
XX  
XX Claim 5; SEQ ID NO 20; 224pp; English.  
PS  
XX The invention relates to a novel isolated GPCR (G-protein coupled  
CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of  
CC the invention demonstrate neuroprotective, nootropic, tranquiliser,  
CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,  
CC antiparkinsonian, cytotstatic, cardiant, hypotensive, antitanginal,  
CC analgesic, anorectic, anti-HIV, antiaethmatic, osteopathic, uropathic,  
CC antituler and antiallergic properties. The nucleic acid molecule and  
CC polypeptide of the invention may be useful in diagnosing, preventing,  
CC treating or ameliorating a medical condition, such as a disorder related  
CC to aberrant G-protein coupled signalling, a disorder related to aberrant  
CC cell cycle regulation, neurological disorders, severe mental retardation  
CC and dyskinesias, brain disorders, spinal cord disorders, affective  
CC disorders, neoplastic disorders, cardiovascular disorders, immunological  
CC disorders, immune-related disorders, endocrinal diseases, growth  
CC disorders, eating disorders, HIV infection, cancers, metabolic disorders  
CC and pituitary disorders. Furthermore, the polynucleotide may be used in  
CC chromosome identification, in identifying organisms from minute  
CC biological samples, in gene therapy or as a molecular weight marker. The  
CC current sequence is that of a human GPCR (G-protein coupled receptor)  
CC protein which was isolated by the method of the invention.  
XX  
XX Sequence 422 AA;  
XX  
Query Match 99.5%; Score 2089; DB 7; Length 422;  
Best Local Similarity 99.3%; Pred. No. 1.3e-208;  
Matches 408; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 MAAPDLLDPKSAQNSKPLRSFTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLII 60  
12 LAAPDLLDPKSAQNSKPLRSFTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLII 71

QY 61 GATVFKALEQPEHSORTTIVIQKTFISQHSVCNSTDDELIIQOIVAAINAGIIPLGNT 120  
DB 72 GATVFKALEQPEHSORTTIVIQKTFISQHSVCNSTDDELIIQOIVAAINAGIIPLGNT 131  
QY 121 SNQISHWDLGSSFPFAGTVITTTIGFNGISPRTEGKIFCIIYVALLGIPILFGFLLAGVGQ 180  
DB 132 SNQISHWDLGSSFPFAGTVITTTIGFNGISPRTEGKIFCIIYVALLGIPILFGFLLAGVGQ 191  
QY 181 LGTIFGKIAKVEDPFIKWNYSQTKIRIISTIIIFLFGCVLFPALPIFKHIEGWSALD 240  
DB 192 LGTIFGKIAKVEDPFIKWNYSQTKIRIISTIIIFLFGCVLFPALPIFKHIEGWSALD 251  
QY 241 AIYFVVIITLTITGFDYVAGGSDIEYLDYFKPVVFWFIIIVGLAYFAAVLSMIGDMLRVIS 300  
DB 252 AIYFVVIITLTITGFDYVAGGSDIEYLDYFKPVVFWFIIIVGLAYFAAVLSMIGDMLRVIS 311  
QY 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVBIYDKFQRTSIRKRLSALAGNNHQ 360  
DB 312 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVBIYDKFQRTSIRKRLSALAGNNHQ 371  
QY 361 ELTPCRRTLSVNHLTNEROVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411  
DB 372 ELTPCRRTLSVNHLTNEROVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 422  
RESULT 9  
AAU07618  
ID AAU07618 standard; protein; 426 AA.  
XX  
XX AAU07618;  
XX  
XX 21-NOV-2001 (first entry)  
XX  
XX Human potassium ion channel TPKC1 protein.  
XX  
XX Transmembrane potassium ion channel protein; inward potassium flux;  
KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
KW insect; TPKC1; human.  
XX  
XX Homo sapiens.  
XX  
XX WO200161006-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 14-FEB-2001; 2001WO-US004680.  
XX  
XX 15-FEB-2000; 2000US-00503849.  
XX  
XX (BADI ) BASF CORP.  
XX  
XX Pausch MH;  
XX  
XX WPI; 2001-536570/59.  
DR N-PSDB; AAS12169.  
XX  
XX New polypeptide, a mutant potassium ion channel protein for improving  
PT inward potassium flux under acidic conditions.  
XX  
XX Example 15; Page 45; 131pp; English.  
XX  
XX The invention relates to a mutant potassium ion channel protein, having  
CC four membrane spanning domains and two pore forming domains, comprising a  
CC mutation at the second pore forming domain. The expression of the mutant  
CC protein in a cell confers improved inward potassium flux and the ability  
CC to grow in the presence of potassium. Mutant proteins and their  
CC corresponding polynucleotide sequences can therefore be used to improve  
CC inward potassium flux into cells under acidic conditions by modulating  
CC the membrane potential using therapeutic agents. The sequences may be  
CC used to develop agonists and antagonists of potassium channel proteins in  
CC order to control pests such as nematodes and insects. This sequence  
CC represents a human transmembrane potassium ion channel protein, TPKC1  
XX



SQ Sequence 426 AA;

Query Match 98.2%; Score 2062; DB 4; Length 426;  
Best Local Similarity 98.5%; Pred. No. 8.5e-206;  
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 60  
DB 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 75

QY 61 GATVPKALEQPEHEISORTTIVIQKTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120  
DB 76 GATVPKALEQPEHEISORTTIVIQKTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135

QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180  
DB 136 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 195

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 255

QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300  
DB 256 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360  
DB 316 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375

QY 361 ELTPCRRRLTSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 411  
DB 376 ELTPCRRRLTSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 426

RESULT 10

AAU07622

ID AAU07622 standard; protein; 426 AA.

AC AAU07622;

DT 21-NOV-2001 (first entry)

DE Human potassium ion channel TPKC1 mutant protein #1.

KW Transmembrane potassium ion channel protein; inward potassium flux;  
KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
KW insect; TPKC1; human; mutant; mutein.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 256 /note= "wild-type Ala replaced by Thr"

FT

XX WO200161006-A2.

PN 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI ) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12181.

XX New polypeptide, a mutant potassium ion channel protein for improving  
PT inward potassium flux under acidic conditions.

XX

PS Claim 37; Page 113-115; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant protein

XX

SQ Sequence 426 AA;

Query Match 98.0%; Score 2058; DB 4; Length 426;  
Best Local Similarity 98.3%; Pred. No. 2.2e-205;  
Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 60  
DB 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 75

QY 61 GATVPKALEQPEHEISORTTIVIQKTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120  
DB 76 GATVPKALEQPEHEISORTTIVIQKTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135

QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180  
DB 136 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 195

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 255

QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300  
DB 256 TIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360  
DB 316 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375

QY 361 ELTPCRRRLTSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 411  
DB 376 ELTPCRRRLTSVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 426

RESULT 11

AAU07623

ID AAU07623 standard; protein; 426 AA.

XX AAU07623;

DT 21-NOV-2001 (first entry)

DE Human potassium ion channel TPKC1 mutant protein #2.

XX Transmembrane potassium ion channel protein; inward potassium flux;  
KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
KW insect; TPKC1; human; mutant; mutein.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"

FT

XX WO200161006-A2.

PN 23-AUG-2001.

PD

XX 14-FEB-2001; 2001WO-US004680.  
 PF 15-FEB-2000; 2000US-00503849.  
 PR (BADI ) BASF CORP.  
 XX Pausch MH;  
 PI WPI; 2001-536570/59.  
 XX N-PSDB; AAS12182.  
 DR New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX Claim 37; Page 115-117; 131pp; English.  
 PS The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein  
 XX Sequence 426 AA;  
 SQ

Query Match 98.0%; Score 2057; DB 4; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 2.8e-205;  
 Matches 404; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAAPDLLPKSAQNSKPRLSFSTKPTVLSRVSDTTINVMKWTSTIFLVVLYLII 60  
 DB 16 VAAPDLLPKSAQNSKPRLSFSTKPTVLSRVSDTTINVMKWTSTIFLVVLYLII 75  
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIPLGNT 120  
 DB 76 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIPLGNT 135  
 QY 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180  
 DB 136 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 195  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGWSALD 240  
 DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGWSALD 255  
 QY 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDMLRVIS 300  
 DB 256 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDMLRVIS 315  
 QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFQRTATSIKKKLSAELAGNHQ 360  
 DB 316 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFQRTATSIKKKLSAELAGNHQ 375  
 QY 361 ELTPCRRTLNVNHLTSDRVLPPLKTESIYINGLTPHCAGBEIAVIENIK 411  
 DB 376 ELTPCRRTLNVNHLTSDRVLPPLKTESIYINGLTPHCAGBEIAVIENIK 426

RESULT 12

AAU07625

ID AAU07625 standard; protein; 426 AA.

XX

XX

XX

XX

DT

XX

DE Human potassium ion channel TPKC1 mutant protein #4.  
 XX Transmembrane potassium ion channel protein; inward potassium flux;  
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human; mutant; muten.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 270  
 FT /note= "Wild-type Gly replaced by Arg"  
 FT  
 XX WO200161006-A2.  
 PN 23-AUG-2001.  
 PD 14-FEB-2001; 2001WO-US004680.  
 PF 15-FEB-2000; 2000US-00503849.  
 PR (BADI ) BASF CORP.  
 XX Pausch MH;  
 PI WPI; 2001-536570/59.  
 DR N-PSDB; AAS12184.  
 DR New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX Claim 37; Page 119-120; 131pp; English.  
 PS The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein  
 XX Sequence 426 AA;  
 SQ

Query Match 97.8%; Score 2054; DB 4; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 5.8e-205;  
 Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MAAPDLLPKSAQNSKPRLSFSTKPTVLSRVSDTTINVMKWTSTIFLVVLYLII 60  
 DB 16 VAAPDLLPKSAQNSKPRLSFSTKPTVLSRVSDTTINVMKWTSTIFLVVLYLII 75  
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIPLGNT 120  
 DB 76 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIPLGNT 135  
 QY 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180  
 DB 136 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 195  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGWSALD 240  
 DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIIFKHIEGWSALD 255  
 QY 241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDMLRVIS 300  
 DB 256 AIYFVVITLTITGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDMLRVIS 315  
 QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFQRTATSIKKKLSAELAGNHQ 360

Db 316 KKTKEVGEFRAHAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLKSLAELAGNHQ 375  
 QY 361 ELTPCRRTLSVNLHNTNRDVLPLPKTESIYLNGLTPHCAGBEIAVNIENIK 411  
 Db 376 ELTPCRRTLSVNLHNTNRDVLPLPKTESIYLNGLAPHCAGBEIAVNIENIK 426

RESULT 13  
 AAU07624  
 ID AAU07624 standard; protein; 426 AA.  
 XX AAU07624;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE Human potassium ion channel TPKC1 mutant protein #3.  
 XX  
 KW Transmembrane potassium ion channel protein; inward potassium flux;  
 KW insect; membrane potential; pesticide; antihelminthic; nematode;  
 XX insect; TPKC1; human; mutant; muten.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"  
 FT Misc-difference 274 /note= "Wild-type Ala replace by Val"  
 FT  
 XX  
 PN WO200161006-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 14-FEB-2001; 2001WO-US004680.  
 XX  
 PR 15-FEB-2000; 2000US-00503849.  
 XX  
 PA (BADI ) BASF CORP.  
 XX  
 PI Pausch MH;  
 XX  
 XX WPI; 2001-536570/59.  
 DR N-PSDB; AAS12183.  
 XX  
 PT New polypeptide, a mutant potassium ion channel protein for improving  
 PT inward potassium flux under acidic conditions.  
 XX  
 PS Claim 37; Page 117-119; 131pp; English.  
 XX  
 CC The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein  
 XX  
 SQ Sequence 426 AA;

Query Match 97.8%; Score 2053; DB 4; Length 426;  
 Best Local Similarity 98.1%; Pred. No. 7.4e-205;  
 Matches 403; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLWVLYLII 60  
 Db 16 VAAPELLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKWTSTIFLWVLYLII 75  
 QY 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIPLGNT 120

Db 76 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIPLGNT 135  
 QY 121 SNQISHWDLGSFFPAGTVTTTIGFNGISPRTEGKIFCIIYALLGIPFLGFLAGVGQ 180  
 Db 136 SNQISHWDLGSFFPAGTVTTTIGFNGISPRTEGKIFCIIYALLGIPFLGFLAGVGQ 195  
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
 Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255  
 QY 241 AIYFVVITLTITIGFDVYAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGLRLVRS 300  
 Db 256 AIYFVVITLTITIGFDVYAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGLRLVRS 315  
 QY 301 KKTKEVGEFRAHAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLKSLAELAGNHQ 360  
 Db 316 KKTKEVGEFRAHAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLKSLAELAGNHQ 375  
 QY 361 ELTPCRRTLSVNLHNTNRDVLPLPKTESIYLNGLTPHCAGBEIAVNIENIK 411  
 Db 376 ELTPCRRTLSVNLHNTNRDVLPLPKTESIYLNGLAPHCAGBEIAVNIENIK 426

RESULT 14  
 AAE10342  
 ID AAE10342 standard; protein; 411 AA.  
 XX AAE10342;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Murine TREK-1 potassium channel protein.  
 XX  
 KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200047738-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
 XX  
 DR WPI; 2000-549146/50.  
 DR N-PSDB; AAD17497.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 PT transfecting cells to be used to identify compounds with anesthetic  
 PT properties.  
 XX  
 PS Claim 9; Page 32-33; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,  
 CC reversible state of unconsciousness with concurrent amnesia and analgesia  
 CC in a mammal upon inhalation. The present sequence is murine TREK-1  
 CC potassium channel protein  
 XX  
 SQ Sequence 411 AA;

Query Match 97.2%; Score 2041; DB 3; Length 411;

[illegible]

RESULT 15

AA28497	AA28497 standard; protein; 411 AA.
ID	XX
XX	XX
XX	AA28497;
XX	XX
XX	12-OCT-1999 (first entry)
DT	XX
XX	XX
DE	Mouse h-TREK1 polypeptide.
XX	XX
XX	h-TREK1; two pore potassium channel; inflammatory disease;
KW	chromosome 1q32.
KW	XX
XX	XX
OS	Mus musculus.
XX	XX
PN	WO9937762-A1.
XX	XX
PD	29-JUL-1999.
XX	XX
XX	02-DEC-1998; 98WO-EP007805.
PF	XX
XX	XX
PR	27-JAN-1998; 98EP-00300570.
PR	09-OCT-1998; 98GB-00022135.
XX	XX
PA	(SMIK ) SMITHLINE BEECHAM PLC.

XX New two pore potassium channel used for, e.g. treatment of cancer,  
PT pulmonary, cardiovascular and inflammatory diseases.

PS Claim 3; Page 26; 44pp; English.

This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1 polynucleotide AA20040. h-TREK1 is a two pore potassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK1 polypeptides. The methods of diagnosis may be used in the treatment of

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 93.9622 Seconds  
(without alignments)  
2239.886 Million cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100

Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNLGTPHCAGEIAVNIENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	2 Q9NRT2	Q9nrt2 homo sapien
2	2079	99.0	411	2 Q8HY88	Q8hy88 bos taurus
3	2062	98.2	426	1 CIW2 HUMAN	Q95069 homo sapien
4	2042	97.2	414	2 Q6P6F9	Q6p6f9 mus musculus
5	2041	97.2	411	1 CIW2 MOUSE	P97438 mus musculus
6	2025	96.4	426	2 Q920B6	Q920b6 rattus norv
7	1254	59.7	538	2 Q6Q834	Q6q834 cryptotlagus
8	1250	59.5	453	2 Q8B2B0	Q8b2b0 m mus muscu
9	1249.5	59.5	535	2 Q8BUW1	Q8buw1 m mus muscu
10	1249	59.5	538	1 CIW4 RAT	Q9j184 rattus norv
11	1243	59.2	538	1 CIW4 HUMAN	P57789 homo sapien
12	1243	59.2	543	2 Q6B014	Q6b014 homo sapien
13	1217.5	58.0	546	2 Q68Y11	Q68ey1 xenopus lae
14	803	38.2	393	1 CIW4 HUMAN	Q9nyg8 homo sapien
15	776.5	37.0	398	1 CIW4 MOUSE	Q84454 mus musculus
16	764.5	36.4	397	2 Q924I4	Q924i4 rattus norv
17	616	29.3	241	2 Q9CX88	Q9cx88 m mus muscu
18	516.5	24.6	152	2 Q6ZW95	Q6zww5 homo sapien
19	502.5	23.9	309	1 CIW6 HUMAN	Q96t55 homo sapien
20	496.5	23.6	294	2 Q6X6Z5	Q6x6z5 homo sapien
21	456	21.7	262	2 Q6X6Z3	Q6x6z3 homo sapien
22	450	21.4	322	2 Q6X6Z4	Q6x6z4 homo sapien
23	432.5	20.6	448	2 Q6PFU3	Q6ptu3 brachydanio
24	427	20.3	499	1 CIW5 HUMAN	Q95279 homo sapien
25	413	19.7	341	2 Q8HZT2	Q8hzt2 bos taurus
26	412.5	19.6	502	2 Q9JK62	Q9jk62 m potassium
27	409.5	19.5	257	2 Q80XE0	Q80xe0 mus musculus
28	406.5	19.4	307	2 Q801T4	Q801t4 xenopus lae
29	400	19.0	184	2 Q8N4V5	Q8n4v5 homo sapien
30	393	18.7	332	1 CIW6 HUMAN	Q96t54 homo sapien
31	380	18.1	336	2 Q8R454	Q8r454 cavia porce

32	379.5	18.1	336	1 CIW1 HUMAN	O00180 homo sapien
33	378.5	18.0	336	2 Q922T2	Q922t2 rattus norv
34	377.5	18.0	336	2 Q99L99	Q99l99 mus musculus
35	372	17.7	331	2 Q8AV15	Q8av15 xenopus lae
36	370.5	17.6	336	1 CIW1 MOUSE	O08581 mus musculus
37	363	17.3	394	1 CIW3_HUMAN	O14649 homo sapien
38	357.5	17.0	365	1 CIW9_CAVPO	Q9j158 cavia porce
39	356.5	17.0	259	2 O02821	O02821 cryptotlagus
40	355	16.9	323	2 Q6PE11	Q6pe11 brachydanio
41	351.5	16.7	396	2 Q923V6	Q923v6 rattus norv
42	349.5	16.6	374	1 CIW9 HUMAN	Q9nnc2 homo sapien
43	348.5	16.6	374	2 Q63ZIO	Q63zi0 xenopus lae
44	348	16.6	313	1 CIW6_HUMAN	Q9y237 homo sapien
45	347.5	16.5	330	1 CIW7_HUMAN	Q9h427 homo sapien

## ALIGNMENTS

RESULT 1

Q9NRT2 PRELIMINARY; PRT; 411 AA.

AC Q9NRT2; DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily K, member 2).

DE K, member 2).

GN Name=TREK-1; Synonyms=KCNK2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]\_SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RX TISSUE=Brain;

RC MEDLINE=20244931; PubMed=10784345;

RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C., Medhurst A.D., Murdock P., Chapman C.G.;

RA "Cloning, localisation and functional expression of the human orthologue of the TREK-1 potassium channel."

RT Pflugers Arch. 439:714-722(2000).

RL [2]\_SEQUENCE FROM N.A.

RN SEQUENCE PCR rescued clones;

RC TISSUE=PCR rescued clones;

RX MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Gruchman J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]\_SEQUENCE FROM N.A.

RP TISSUE=PCR rescued clones;

RA Strausberg R.;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

[illegible]

```

RESULT 2
Q8HY88
ID Q8HY88 PRELIMINARY; PRT; 411 AA.
AC Q8HY88;
DT 01-MAR-2003 ('TREMBlrel. 23, Created)
DT 01-MAR-2003 ('TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 ('TREMBlrel. 25, Last annotation update)
DE Potassium channel subfamily K member 2.
GN Name=Kcnk2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Adrenal cortex;
RC MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;
RA Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
RT "An ACTH- and ATP-regulated background K+ channel in adrenocortical
RT cells is TREK-1."
RL J. Biol. Chem. 277:49186-49199 (2002).
RC -I- SIMILARITY: Belongs to the two pore domain potassium channel
      (TC 1.A.1.8) family.
DE EMBL: AY148474; AAN37591.1; -.

```

DR	GO: 0016021; C: integral to membrane; IEA.	
DR	GO: 0005216; F: ion channel activity; IEA.	
DR	GO: 0005267; F: potassium channel activity; IEA.	
DR	GO: 0006811; P: ion transport; IEA.	
DR	GO: 0006813; P: potassium ion transport; IEA.	
DR	InterPro: IPR003280; K+ channel 2 pore.	
DR	InterPro: IPR001622; K+ channel_pore.	
DR	InterPro: IPR003976; Trek channel.	
DR	PRINTS: PRO1333; 2PORECHANNEL.	
DR	PRINTS: PRO1499; TREKCHANNEL.	
KW	Ion transport; Ionic channel; Transmembrane; Transport.	
SQ	SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;	
	Query Match	99.08; Score 2079; DB 2; Length 411;
	Best Local Similarity	99.08; Pred. No. 2e-132; Indels 0; Gaps
	Matches 407; Conservative 2; Mismatches 2;	
Qy	1	MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTVTSTIFLVVYLII
Db	1	MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTVTSTIFLVVYLYI
Qy	61	GATVFKALEQPEHSQRTTIVIOKQTFISQHSQNSWSTELDELIQIQVAAINAGIPIPLGN
Db	61	GATVFKALEQPEHSQRTTIVIOKQTFISQHSQNSWSTELDELIQIQVAAINAGIPIPLGN
Qy	121	SNQISHWDLGSSFFAGTVITTTIGFNGNI SPRTEGGKIFCIIYALLGILPFGFLLAGVGD
Db	121	SNQISHWDLGSSFFAGTVITTTIGFNGNI SPRTEGGKIFCIIYALLGILPFGFLLAGVGD
Qy	181	LGTIFGKGIKAVETDFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHISGWSAL
Db	181	LGTIFGKGIKAVETDFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHISGWSAL
Qy	241	AIYFVVIITLTITGFDYVAGGSDIEYLDYFKVPVWFILVGLAYFAAIVLSMIGDMLRVI
Db	241	AIYFVVIITLTITGFDYVAGGSDIEYLDYFKVPVWFILVGLAYFAAIVLSMIGDMLRVI
Qy	301	KKTKEEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKPKLSAELAGNHNI
Db	301	KKTKEEVEGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSIKPKLSAELAGNHNI
Qy	361	ELTPCRRTLTSNVHLTNERDVLPLLLKTESIYINGLTPPHCAGEEIAVENIK 411
Db	361	ELTPCRRTLTSNVHLASRDVLPLLLKTESIYINGLTPPHCAGEEIAVENIK 411

```

RESULT 3
CIN2_HUMAN
ID      CIN2_HUMAN      STANDARD;      PRT;      426 AA.
AC      Q95069; Q9UN63;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Potassium channel subfamily K member 2 (Outward rectifying potassium
DE      channel protein TREK-1) (TREK-1 K+ channel subunit) (two-pore
DE      potassium channel TPKC1).
GN      Name=KCNK2; Synonyms=TREK, TREK1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
RA      Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT      "Inhalational anesthetics activate two-pore-domain background K+
RT      channels."
RT      Nat. Neurosci. 2:422-436(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Price L.A., Hellings S.E., Hayaishi J.H., Pausch M.H.;
RL      Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

```

CC -!- FUNCTION: Outward rectifying potassium channel.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- MISCELLANEOUS: Activated by volatile general anaesthetics such as  
 CC chloroform, halothane and isoflurane.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AF129399; RAD47569.1; --  
 CC EMBL; AF004711; AD01203.1; --  
 CC Genew; HGNC:6277; KCNK2.  
 CC MIM; 603219; --  
 CC GO; GO:0016020; C:membrane; NAS.  
 CC GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.  
 CC GO; GO:0008813; P:potassium ion transport; NAS.  
 CC InterPro; IPR003280; K+channel\_2pore.  
 CC InterPro; IPR001622; K+channel\_pore.  
 CC InterPro; IPR003976; Trek channel.  
 CC PRINTS; PR01333; 2POREKCHANEL.  
 CC PRINTS; PR01499; TREKCHANNEL.  
 CC Glycoprotein; Ion transport; Ionic channel; Potassium;  
 CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 KW DOMAIN 1 61 Cytoplasmic (Potential).  
 FT TRANSMEM 62 82 Potential.  
 FT DOMAIN 144 170 Pore-forming 1 (Potential).  
 FT TRANSMEM 172 192 Potential.  
 FT DOMAIN 193 223 Cytoplasmic (Potential).  
 FT TRANSMEM 224 244 Potential.  
 FT DOMAIN 253 283 Pore-forming 2 (Potential).  
 FT TRANSMEM 288 308 Potential.  
 FT DOMAIN 309 426 Essential for chloroform and halothane  
 FT sensitivity (By similarity).  
 FT DOMAIN 354 426 Required for basal channel activity (By  
 FT similarity).  
 FT CARBOHYD 110 110 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 134 134 N-linked (GlcNAc. .) (Potential).  
 FT CONFLICT 2 16 Missing (in Ref. 2).  
 FT CONFLICT 309 311 RLV -> DWL (in Ref. 2).  
 FT CONFLICT 391 391 S -> N (in Ref. 2).  
 FT CONFLICT 411 411 A -> T (in Ref. 2).  
 FT SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;  
 SQ  
 Query Match 98.2%; Score 2062; DB 1; Length 426;  
 Best Local Similarity 98.5%; Pred. No. 3e-131;  
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAAPDLDDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLI 60  
 Db :|||||  
 QY 16 VMAPDLDDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLI 75  
 Db :|||||  
 QY 61 GATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELQIQAIAINAGIIPLGNT 120  
 Db 76 GATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELQIQAIAINAGIIPLGNT 135  
 QY 121 SNOISHWDLGSSFFPAGTIVITTFGNISPRTEGGKIFCLIIYALLGPIPLFGLLAGVGQ 180  
 Db 136 SNOISHWDLGSSFFPAGTIVITTFGNISPRTEGGKIFCLIIYALLGPIPLFGLLAGVGQ 195  
 QY 181 LGTIFGKIAKVEDTIFKNVSTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240  
 Db 196 LGTIFGKIAKVEDTIFKNVSTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 255  
 QY 241 AIYFVWITLTITGFDYVAGGSDIEYLDYKPVVFWFVILGLAYFAAIVLSMIGLRLVRVIS 300  
 Db :|||||

Db 256 AIYFVWITLTITGFDYVAGGSDIEYLDYKPVVFWFVILGLAYFAAIVLSMIGLRLVRVIS 315  
 QY 301 KKTKEEVEGFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIKRLKSLAELAGNNHQ 360  
 Db :|||||  
 QY 316 KKTKEEVEGFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIKRLKSLAELAGNNHQ 375  
 Db :|||||  
 QY 361 ELTPCRRTLSVNNHLTNERDVLPLPKTESIYINGLTTPHCAGEEIAVIEINIK 411  
 Db 376 ELTPCRRTLSVNNHLTNERDVLPLPKTESIYINGLTTPHCAGEEIAVIEINIK 426  
 Db :|||||  
 RESULT 4  
 Q6P6P9 PRELIMINARY; PRT; 414 AA.  
 AC Q6P6P9; DT 05-JUL-2004 (TREMELrel. 27, Created)  
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
 DE Kcnk2 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RC Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC EMBL; BC062094; AAH62094.1; --  
 CC GO; GO:0016021; C:integral to membrane; TAS.  
 CC GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.  
 CC GO; GO:0005249; P:voltage-gated potassium channel activity; IDA.  
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.  
 CC GO; GO:0006813; P:potassium ion transport; IDA.  
 CC GO; GO:0030322; P:stabilization of membrane potential; TAS.  
 CC InterPro; IPR003280; K+channel\_2pore.  
 CC InterPro; IPR001622; K+channel\_pore.  
 CC InterPro; IPR003976; Trek channel.  
 CC PRINTS; PR01333; 2POREKCHANEL.  
 CC PRINTS; PR01499; TREKCHANNEL.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 SQ SEQUENCE 414 AA; 45555 MW; 27F52D51DFFC66F8 CRC64;

Query Match 97.2%; Score 2042; DB 2; Length 414;  
 Best Local Similarity 96.1%; Pred. No. 6.5e-130;  
 Matches 395; Conservative 13; Mismatches 3; Indels 0; Gaps 0;







```

Db      361 ELTPCRTLNVNHLTSEREVLPLLKAEISYLNGLTPHCAEDIAVIENWK 411

RESULT 6
Q920B6
ID Q920B6 PRELIMINARY; PRT; 426 AA.
AC Q920B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2p domain potassium channel: KCNK2 (Tandem pore domain potassium
DE channel TREK-1) (Arachidonic acid sensitive tandem pore domain
DE potassium channel).
DE Name=Kcnk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11319556;
RA Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT voltage-dependent channel.";
RL Nat. Neurosci. 4:486-491(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11897838;
RA Gu W., Schlichtchortl G., Hirsch J.R., Engels H., Karschin C.,
RA Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice
RT variants of the two-pore-domain potassium channel TREK-2.";
RL J. Physiol. 539:657-668(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11897838;
RA Li Z.B., Wang X.L.;
RT "Possible role of TREK-1 in temperature regulation.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC EMBL; AF325671; AAL01159.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR EMBL; AF385402; AAL95708.1; -.
DR EMBL; AF695826; RAU06141.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR PRINTS; PR01333; 2POREKCHANEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 426 AA; 46912 MW; CACDA05B8E95FDBC CRC64;

Query Match 96.4%; Score 2025; DB 2; Length 426;
Best Local Similarity 95.4%; Pred. No. 9.4e-129;
Matches 392; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYII 60
Db      16 VAAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYII 75
QY 61 GATVFKALPQPEISORTTIVIOKQTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120
Db      76 GATVFKALPQPEISORTTIVIOKQNFIAQACVNSTELDELIQOIVAAINAGIPLGNN 135
QY 121 SNOISHWDLGSGFFAGTITIGFNGISPRTEGGKIFCIIVALLGIPFGFLAGVGDQ 180
Db      136 SNOVSHWDLGSGFFAGTITIGFNGISPRTEGGKIFCIIVALLGIPFGFLAGVGDQ 195
QY 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240

```

```

Db      196 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 255
QY 241 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVVWFVWILVGLYFAAVLSMIGDWLRVIS 300
Db      256 AIYFVVITLTITIGFDYVAGGSDIEYLDYFKPVVWFVWILVGLYFAAVLSMIGDWLRVIS 315
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVETIDYKFORATSIKRKLASLAGHNQ 360
Db      316 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVETIDYKFORATSIKRKLASLAGHNQ 375
QY 361 ELTPCRTLNVNHLTNERDVLPLLKTESIYLNGLTPHCAEDIAVIENIK 411
Db      376 ELTPCRTLNVNHLTSEREVLPLLKAEISYLNGLTPHCAEDIAVIENWK 426

RESULT 7
Q60834
ID Q60834 PRELIMINARY; PRT; 538 AA.
AC Q60834;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Potassium channel TREK-2.
DE Name=KCNK10;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC EMBL; AY553324; AAS66991.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; TREK channel.
DR PRINTS; PR01333; 2POREKCHANEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 538 AA; 59844 MW; 1F06C8EA0DE8CB4D CRC64;

Query Match 59.7%; Score 1254; DB 2; Length 538;
Best Local Similarity 63.7%; Pred. No. 1.4e-76;
Matches 247; Conservative 56; Mismatches 63; Indels 22; Gaps 6;

QY 2 AAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYII 56
Db      23 AAPPYCQPKSATNGHPAPRLSISRATVVA-RMEGTSGGQSQVNMKWTVAIFVWV 81
QY 57 YLIIGATVPKALEQPEISORTTIVIOKQTFISQHSVNSTELDELIQOIVAAINAGIIP 116
Db      82 YLVTGGLVFRALQPESSQKNTIALEKAEFRDHCVSPQBLETLIQHALDADNAGVSP 141
QY 117 LGNTSNOISHWDLGSGFFAGTITIGFNGISPRTEGGKIFCIIVALLGIPFGFLAG 176
Db      142 ICGNSNNSSHWDLGSGFFAGTITIGYGNIAAPSTEGGKIFCIIVALLGIPFGFLAG 201
QY 177 VGDQLTGTFGKGIKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEG 236
Db      202 IGDQLTGTFGKGIKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEG 261
QY 237 SALDAIYFVWITLTITIGFDYVAGG-SDIEYLDYFKPVVWFVWILVGLYFAAVLSMIGDW 295
Db      262 TALESIYFVWITLTITIGFDYVAGGAGNINYEYKPLVWFWILVGLYFAAVLSMIGDW 321
QY 296 LRVISKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVETIDYKFORATSIKRKLASLAG 355

```



DE 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuura T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC EMBL: AK082153; BAC38424.1; -.

DR GO: GO:0016021; C: integral to membrane; IEA.

DR GO: GO:0005216; F: ion channel activity; IEA.

DR GO: GO:0005267; F: potassium channel activity; IEA.

DR GO: GO:0006911; P: ion transport; IEA.

DR GO: GO:0006913; P: potassium ion transport; IEA.

DR InterPro: IPR001280; K+ channel 2pore.

DR InterPro: IPR001622; K+ channel 2pore.

DR InterPro: IPR003976; Trek channel.

DR PRINTS: PR01333; 2POREKCHANNEL.

DR PRINTS: PR01499; TREKCHANNEL.

KW ion transport; ionic channel; Transmembrane; Transport.

SQ SEQUENCE 535 AA; 59401 MW; 3E9BE89F875C26BD CRC64;

Query Match 59.5%; Score 1249.5; DB 2; Length 535;

Best Local Similarity 59.3%; Pred. No. 2.8e-76;

Matches 252; Conservative 61; Mismatches 77; Indels 35; Gaps 7;

QY 2 AAPDLLDPKSA--AQNKPRLSPSTKPTVLASVESDT---TINVNMKVTSTIFLVVL 56

DB 20 AAPVCPQKSAATNGHPVPRLSISSRATVVA-RMEGASQGLQTVMKWKTVAIFV 78

QY 57 YLIIGATVPKALPEPHEISORTTIVIOKOTFISQHSVNSTELDELIQIIVAINAGIIP 116

DB 79 YLVGTGLVFRALPEQPFESSQKNTIALEKAEFLRDHICVSPQELDTIQHALDADNAGVSP 138

QY 117 LGNTSNOISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAG 176

DB 139 VGNSSNSSSHWDLGSAFFAGTVITIGYGNIASTEGGKIFCIIYALFIPFGFLLAG 198

QY 177 VGDQLGTIFKGIKVEDTFIKMNVSTQKIRIISTIFILFGCVLFPALPFIKHIKIEGW 236

DB 199 IGDQLGTIFGKSIARVEKVRKQVSTQKIRVISTIFILAGCIVFTIPAVIFKYEIGW 258

QY 237 SALDAIFYVITLTITIGPDYVAGG-SDIEYLDYFYPVWFWILVGLAYFAAVLSMIGDW 295

DB 259 TALESIYFVVTLTITVFGDFVAGNAGINRYEYKPLVWFWILVGLAYFAAVLSMIGDW 318

QY 296 LRVISKTKKEEVEGEPRAHAAEWNTAVTAEFKETRRRLSVEIYDKFORATSI----KKKLS 351

DB 319 LRVLSTKTKKEEVEIKAAHAEKAVNTAEFRTRRLSVEIHDKQRAATIRSMERRRLG 378

QY 352 AELAGNHNLTPCRRTL-----SVNHLTNERDVLPLPLKTESIYLNGLT 396

DB 379 LDQRAHSLDWLSPKRSVFAALDTGRFKASSQBSINRPNLRLKGP-----EQLT 429

QY 397 PHCAG 401

DB 430 KHGGQ 434

RESULT 10

CIWA\_RAT STANDARD; PRT; 538 AA.

ID CIWA\_RAT

AC Q9JIS4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).

GN Names=Kcnk10; Synonyms=Trek2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=101116;

SEQUENCE FROM N.A.

RX MEDLINE=20298807; PubMed=10747911; DOI=10.1074/jbc.M000445200;

RA Wang H., Kim Y., Kim D.;

RT TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family.";

RL J. Biol. Chem. 275:17412-17419(2000).

CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen,

CC and testis.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF196965; AAF75132.1; -;  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek\_channel.  
 DR PRINTS; PRO1333; 2POREKCHANEL.  
 DR PRINTS; PRO1499; TREKCHANNEL.  
 KW Glycoprotein; Ion transport; Transmembrane; Transport; Potassium;  
 KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.  
 FT DOMAIN 1 71 Cytoplasmic (Potential).  
 FT TRANSMEM 72 92 Potential.  
 FT DOMAIN 154 180 Pore-forming 1 (Potential).  
 FT TRANSMEM 182 202 Potential.  
 FT DOMAIN 203 233 Cytoplasmic (Potential).  
 FT TRANSMEM 234 254 Potential.  
 FT DOMAIN 263 294 Pore-forming 2 (Potential).  
 FT TRANSMEM 299 319 Potential.  
 FT DOMAIN 320 538 Cytoplasmic (Potential).  
 FT CARBOHYD 144 144 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 147 147 N-linked (GlcNAc . .) (Potential).  
 SEQUENCE 538 AA; 59800 MW; 1FF33FOAA52B97E4 CRC64;  
 Query Match 59.5%; Score 1249; DB 1; Length 538;  
 Best Local Similarity 63.7%; Pred. No. 3.1e-76;  
 Matches 247; Conservative 55; Mismatches 64; Indels 22; Gaps 6;  
 QY 2 AAPDLLDPKSA--AQNKKRLSFSKPTVLASRVESDT---TINVMKKWTSTIFLVVVL 56  
 DB 23 AAPVCQPKSATNGHHVPVRLSSISRTATVVA-RMEGASQGGIQTVMKKVTVAIFVVVV 81  
 QY 57 YLIIGATVPKALEQHEISQRTTIVIQOTFTISQHSVCNSTDDELIIQOIVAAINAGIIP 116  
 DB 82 YLVTVGLVFRALQEPSSQKNTALEKAEFLRDHICVSPQELTILQHALDADNAGVSP 141  
 QY 117 LGNTSNQIHWDLGSSFFPAGTVITIGFGNISPRTEGKIFCIYIALLGIPLFGFLAG 176  
 DB 142 VGNSSNSSHWDLGSAFFPAGTVITIGYGNIAPESTEGKIFCIYIAPLFGFLAG 201  
 QY 177 VGDOLGTIFGKIAGVEDTFIKWYSOTKIRIISITIFILFGCVLVALPAIFKHIEGW 236  
 DB 202 IGDQLGTIFGKSIARVEKVRKQVSGTKIRIVISITILFGLACIVFVITPAVIFKIEGW 261  
 QY 237 SALDAIFYFVITLTITIGFDYVAGG-SDIEYLDYFKPVVWFVILVGLAYFAAFLSMIGDW 295  
 DB 262 TALESIYFVITLTITIGFDYVAGGAGNINYEYKPLVFWILVGLAYFAAFLSMIGDW 321  
 QY 296 LRVISKKTKEEVEGFAHAAEWANTVATFETRRRLSVEIYDKFQRTATSIKKLSAEILA 355  
 DB 322 LRVLSKKTKEEVEGFAHAAEWANTVATFETRRRLSVEIYDKFQRTATSIKKLSAEILA 376  
 QY 356 GNNHQLTFCRRLTSVNHLTNEDVLP 383  
 DB 377 -----RRRLGLDQRAHSLDMLSP 394  
 RESULT 11  
 ID CIWA HUMAN STANDARD; PRT; 538 AA.  
 AC P57789; Q8TDK7; Q9HB59;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 10 (Outward rectifying potassium  
 DE channel TREK-2) (TREK-2 K+ channel subunit).  
 GN Name=KCNK10; Synonyms=TREK2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=20435789; PubMed=1080510; DOI=10.1074/jbc.M002822200;  
 RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;  
 RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple  
 RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,  
 RT Gi, and Gq protein-coupled receptors."; *fed date*  
 RL J. Biol. Chem. 275:28398-28405(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS B AND C).  
 RX MEDLINE=21896087; PubMed=11897838;  
 RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,  
 RA Karschin A., Derst C., Steinlein O.K., Daut J.;  
 RT "Expression pattern and functional characteristics of two novel splice  
 RT variants of the two-pore-domain potassium channel TREK-2."; *fed date*  
 RL J. Physiol. (Lond.) 539:657-668(2002).  
 CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
 CC activating and non-inactivating outward rectifier K(+) currents.  
 CC Activated by arachidonic acid and other naturally occurring  
 CC unsaturated free fatty acids.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Name=A; Synonyms=TREK-2a;  
 CC IsoId=P57789-1; Sequence=Displayed;  
 CC Name=B; Synonyms=TREK-2b;  
 CC IsoId=P57789-2; Sequence=VSP\_006697;  
 CC Name=C; Synonyms=TREK-2c;  
 CC IsoId=P57789-3; Sequence=VSP\_006698;  
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney  
 CC and to a lower level in brain, testis, colon, and small intestine.  
 CC Isoform b is strongly expressed in kidney (primarily in the  
 CC proximal tubule) and pancreas, whereas isoform c is abundantly  
 CC expressed in brain.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC (TC 1.A.1.8) family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF279890; AAG15191.1; -;  
 DR EMBL; AF385399; AAL95705.1; -;  
 DR EMBL; AF385400; AAL95706.1; -;  
 DR Genew; HGNC:6273; KCNK10.  
 DR MIM; 605873; -;  
 DR GO; GO:0005267; F:potassium channel activity; TAS.  
 DR GO; GO:0006810; P:transport; TAS.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek\_channel.  
 DR PRINTS; PRO1333; 2POREKCHANEL.  
 DR PRINTS; PRO1499; TREKCHANNEL.  
 KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;  
 KW Potassium; Potassium channel; Transmembrane; Transport;  
 KW Voltage-gated channel.  
 FT DOMAIN 1 71 Cytoplasmic (Potential).  
 FT TRANSMEM 72 92 Potential.  
 FT DOMAIN 154 180 Pore-forming 1 (Potential).  
 FT TRANSMEM 182 202 Potential.  
 FT DOMAIN 203 233 Cytoplasmic (Potential).  
 FT TRANSMEM 234 254 Potential.

```

FT DOMAIN 263 284 Pore-forming 2 (Potential).
FT TRANSMEM 299 319 Potential.
FT DOMAIN 320 538 Cytoplasmic (Potential).
FT CARBOHYD 144 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 12 MFELYDFFLSL -> MKGDRTEGCKRSDS (in isoform B).
FT FTID=VSP 006697.
FT VARSPLIC 1 12 MFELYDFFLSL -> MKFPIETPRKQVNWDPK (in isoform C).
FT FTID=VSP 006698.
FT CONFLICT 529 529 E -> G (in Ref. 2).
FT SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 59.2%; Score 1243; DB 1; Length 538;
Best Local Similarity 62.7%; Pred. No. 7.9e-76;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNSKPLRSFSTKPTVLASRVESDT---TINVMKWKTVSTI 50
Db 17 AAAPVCQPKSATNGOPPAPAPTPTPLRSISSRATVVA-RMEGTSGGLQTVMKWKTVAI 75
QY 51 FLAVVYLIIIGATVFKALEQPHISQRTTIVIQKTFISQHSVNSTELDELIQIVAAI 110
Db 76 FVVVVVYLTGVLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
QY 111 NAGIIPLGNTSNQISHWDLGSGFFAGTVITIGFNGISPRTEGGKIFCIIYALLGIPLF 170
Db 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITIGYGNIAPSSTEGGKIFCIIYALLGIPLF 195
QY 171 GFLLAGVGDLQGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAIF 230
Db 196 GFLLAGIGDLQGTIFGKSIARVEKVFRRKQVSTQKIRVISTITILFAGCIVFVTPAVIF 255
QY 231 KHIEGWSALDAIFYVVTITLTIGFGDYVAGG-SDIEYLDYKPVVFWFVLVGLAYFAAVL 289
Db 256 KYIEGWTALIESIFYVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVLVGLAYFAAVL 315
QY 290 SMIGDMLRVISKKTKEEVEGEFRAHAAEWNTANTAEFKETRRLRSVEIYDKFORATSIRK 349
Db 316 SMIGDMLRVISKKTKEEVEGEIKAHAAEWKANTAEFRTRRLRSVEIHDKQRAATIR-- 373
QY 350 LSAELAGNHNQBELTFCRRTLTSVNHITNDRDLPP 383
Db 374 -SME-----RRRLGDLQRAHSLDMLSP 394

RESULT 12
Q6B014 PRELIMINARY; PRT; 543 AA.
AC Q6B014;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Potassium channel, subfamily K, member 10, isoform 3.
GN Name=KCNK10;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max3S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

```

```

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075022; AAH75022.1; -
DR EMBL; BC075021; AAH75021.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001822; K+channel_pore.
DR InterPro; IPR011255; N1r Siralpa_1/3.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
DR Ionic channel.
KW IONIC CHANNEL.
SQ SEQUENCE 543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;

Query Match 59.2%; Score 1243; DB 2; Length 543;
Best Local Similarity 62.7%; Pred. No. 7.9e-76;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNSKPLRSFSTKPTVLASRVESDT---TINVMKWKTVSTI 50
Db 22 AAAPVCQPKSATNGOPPAPAPTPTPLRSISSRATVVA-RMEGTSGGLQTVMKWKTVAI 80
QY 51 FLAVVYLIIIGATVFKALEQPHISQRTTIVIQKTFISQHSVNSTELDELIQIVAAI 110
Db 81 FVVVVVYLTGVLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 140
QY 111 NAGIIPLGNTSNQISHWDLGSGFFAGTVITIGFNGISPRTEGGKIFCIIYALLGIPLF 170
Db 141 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITIGYGNIAPSSTEGGKIFCIIYALLGIPLF 200
QY 171 GFLLAGVGDLQGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAIF 230
Db 201 GFLLAGIGDLQGTIFGKSIARVEKVFRRKQVSTQKIRVISTITILFAGCIVFVTPAVIF 260
QY 231 KHIEGWSALDAIFYVVTITLTIGFGDYVAGG-SDIEYLDYKPVVFWFVLVGLAYFAAVL 289
Db 261 KYIEGWTALIESIFYVVTITLTIGFGDYVAGGSDIEYLDYKPVVFWFVLVGLAYFAAVL 320
QY 290 SMIGDMLRVISKKTKEEVEGEFRAHAAEWNTANTAEFKETRRLRSVEIYDKFORATSIRK 349
Db 321 SMIGDMLRVISKKTKEEVEGEIKAHAAEWKANTAEFRTRRLRSVEIHDKQRAATIR-- 378
QY 350 LSAELAGNHNQBELTFCRRTLTSVNHITNDRDLPP 383
Db 379 -SME-----RRRLGDLQRAHSLDMLSP 399

RESULT 13
Q68EY1 PRELIMINARY; PRT; 546 AA.
AC Q68EY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC46288 protein (Fragment).

```

Qy	257	YVAGG-SDIEYLDPKPWFWFWILVGLAYFAAVLSMIGDWLRLVISKTKKEEVEGEPAAHAA	311
Db	292	FVAGGNTDISYREYKPLWFWILVGLAYFAAVLSMIGDWLRLVISKTKKEEVEGEEKAHAA	351
Qy	316	EWTAIVTAEFKTRRRRLSVEIYDKFORATSIKRLKLSAELAGNHNQELTPCRRTLSTVNHULT	375
Db	352	EKWANVTARETRRRRLSVEIYDKFORATSIKRLKLSAELAGNHNQELTPCRRTLSTVNHULT	375
Qy	376	NERDVLPP 383	
Db	397	HSLDMLSP 404	

RESULT 14  
 CIW4 HUMAN  
 ID CIW4 HUMAN STANDARD; PRT; 393 AA.  
 AC Q9NYG8; Q96T94;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-stimulated potassium channel protein) (TAAK) (Two pore K+ channel Kt4.1).  
 DE  
 GN Name=KCNK4; Synonyms=TAAK;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RC PubMed=110423259; DOI=10.1016/S0169-328X(00)00183-2;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;  
 RA "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel.";  
 RT Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RL [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Frontal cortex;  
 RA Gray A.T.;  
 RA "Assignment of KCNK4 encoding the human potassium channel TAAK to chromosome 11.";  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC MEDLINE=40231699; PubMed=10767409; DOI=10.1016/S0014-5793(00)01388-0;  
 RA Lesage F., Maingret F., Lazdunski M.;  
 RA "Cloning and expression of human TAAK, a polyunsaturated fatty acids-activated and mechano-sensitive K(+) channel.";  
 RT FEBS Lett. 471:137-140(2000).  
 RL [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC MEDLINE=42178385; PubMed=12911490; DOI=10.1016/S0169-328X(02)00157-2;  
 RA Ozaita A., Vega-Saenz de Miera E.;  
 RA "Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCNK4. Chromosomal localization, tissue distribution and functional expression.";  
 RT Brain Res. Mol. Brain Res. 102:18-27(2002).  
 RL [5]  
 RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).  
 RC PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
 RA Hillman R.T., Green R.E., Brenner S.E.;  
 RA "An unappreciated role for RNA surveillance.";  
 RT Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).  
 CC -!- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying potassium channel. Outward rectification is reversed at high external K(+) concentrations (By similarity).  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Kt4.1a;



```
CC      IsoId=Q9NYG8-1; Sequence=Displayed;
CC      Name=2; Synonyms=KT4.1b;
CC      IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC      Notes=May be produced at very low levels due to a premature stop
CC      codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC      -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC      (TC 1.A.1.8) family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF248242; AAG31731.1; -
CC      EMBL; AF247042; AAF64062.1; ALT_INIT.
CC      EMBL; AF259500; AAK49389.1; -
CC      EMBL; AF259501; AAK49390.1; -
CC      Genew; HGNC:6279; KCNK4.
CC      MIM; 605720; -
CC      GO; GO:005267; F.potassium channel activity; TAS.
CC      GO; GO:0006813; P.potassium ion transport; TAS.
CC      InterPro; IPR003280; K+channel_2pore.
CC      InterPro; IPR001622; K+channel_pore.
CC      InterPro; IPR008074; TRAAK channel.
CC      PRINTS; PR01333; 2POREKCHANNEL.
CC      PRINTS; PR01691; TRAAKCHANNEL.
CC      Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW      Potassium; Potassium channel; Transmembrane; Transport;
KW      Voltage-gated channel.
FT      DOMAIN 1 3 Cytoplasmic (Potential).
FT      TRANSMEM 4 24 Potential.
FT      DOMAIN 89 113 Pore-forming 1 (Potential).
FT      TRANSMEM 118 138 Potential.
FT      DOMAIN 139 171 Cytoplasmic (Potential).
FT      TRANSMEM 172 192 Potential.
FT      DOMAIN 197 221 Pore-forming 2 (Potential).
FT      TRANSMEM 234 254 Potential.
FT      DOMAIN 255 393 Cytoplasmic (Potential).
FT      CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).
FT      VARSPLIC 1 1 M -> MTTAQPEPPARPLQAGSGAGPAPGRAM (in
FT      isoform 2).
FT      /FTId=VSP_006689.
FT      P -> L (in Ref. 2).
FT      CONFLICT 328 328 P -> L (in Ref. 2).
FT      SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;
FT
FT      Query Match 38.2%; Score 803; DB 1; Length 393;
FT      Best Local Similarity 51.1%; Pred. No. 3e-46;
FT      Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY      42 MKWKTSTFVLVVLVLIIGATVFKALEPHEISQRTTIVQKTFISQHSVNSTELDE 101
Db      1 MRSTTLALLALLVLLVSGALVFRALEQPEHQEAQRELGEVREKFLRAHPCVSDQELG 60
QY      102 LIQQTVAALNAGIIPLGNTSNQISH--WDLGSSFFPAGTVITIGFNSIPRTEGKIFC 159
Db      61 LIKEVADALGGGADPNTNSTSSSHSADWLGSAFFSFGTIITIGYGNVALRTDAGRLFC 120
QY      160 IYVALLGIPFLGALLAGVGDLGTIFGKIAKVEDTFIKWVYSQTKIRIISTIFLFGC 219
Db      121 IFVALVGIPFLGALLAGVGDLGSSLRHGIGHIEALFLKWHVPPELVRLVLSMLFLIGC 180
QY      220 VLFVALPAIFKHIEGSSALDAIFYFVITLITIGFGDYVAGGSDIYELDFYKPVVWFIL 279
Db      181 LLFVLTPTFVFCYMEDSKLEALFYFVITLITIGFGDYVAGADPRDPSPAYQLVWFIL 240
QY      280 VGLAYFAAVLSMTGDLNRLVSKTKKEVEGFRAHAAEWANTVA 323
Db      241 LGLAYFASVLTITGNLRLVSRTRAEMLGSLTAQAASWTGTVA 284
```

```
RESULT 15
CIW4 MOUSE
ID CIW4 MOUSE STANDARD; PRT; 398 AA.
AC O88454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE stimulated potassium channel protein) (TRAAK).
GN Name=Kcnk4; Synonyms=TRAAK;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98292450; PubMed=9628867; DOI=10.1093/emboj/17.12.3297;
RA Pink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.;
RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT polyunsaturated fatty acids.";
RN [2]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
RA Patel A.J., Honore E., Lesage F., Pink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426 (1999).
CC -1- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying
CC potassium channel. Outward rectification is reversed at high
CC external K(+) concentrations.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O88454-1; Sequence=Displayed;
CC Name=2; Synonyms=TRAAKT, Truncated;
CC IsoId=O88454-2; Sequence=VSP_006690, VSP_006691;
CC -1- TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not
CC detected in heart, skeletal muscle, liver, lungs, kidney and
CC testis.
CC -1- MISCELLANEOUS: Activated by arachidonic acid and other unsaturated
CC fatty acids. Not affected by volatile general anaesthetics such as
CC chloroform, diethyl ether, halothane and isoflurane.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF056492; AAC40181.1; -
CC      MGD; MGI:1298234; Kcnk4.
CC      InterPro; IPR003280; K+channel_2pore.
CC      InterPro; IPR001622; K+channel_pore.
CC      InterPro; IPR008074; TRAAK channel.
CC      PRINTS; PR01333; 2POREKCHANNEL.
CC      PRINTS; PR01691; TRAAKCHANNEL.
CC      Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW      Potassium; Potassium channel; Transmembrane; Transport;
KW      Voltage-gated channel.
FT      DOMAIN 1 3 Cytoplasmic (Potential).
FT      TRANSMEM 4 24 Potential.
FT      DOMAIN 89 113 Pore-forming 1 (Potential).
FT      TRANSMEM 119 139 Potential.
```

```
FT DOMAIN 140 171 Cytoplasmic (Potential).
FT TRANSMEM 172 192 Potential.
FT DOMAIN 198 222 Pore-forming 2 (Potential).
FT TRANSMEM 235 255 Potential.
FT DOMAIN 256 398 Cytoplasmic (Potential).
FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 84 84 N-linked (GlcNAc. .) (Potential).
FT VARSPLIC 63 67 KILVE -> KAMAI (in isoform 2).
FT VARSPLIC 68 398 /FTid=VSP 006690.
FT VARSPLIC 68 398 Missing (in isoform 2).
FT VARSPLIC 68 398 /FTid=VSP 006691.
SQ SEQUENCE 398 AA; 43051 NW; 478A834B7B7AEC92 CRC64;

Query Match 37.0%; Score 776.5; DB 1; Length 398;
Best Local Similarity 49.8%; Pred. No. 1.9e-44;
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;

QY 42 MKWKTIVSTIFLVVLYLIIGATVFKALQPHQHEISQRTTIVIQKQTFISQHSQVNSTELDE 101
Db 1 MRSITLLALLLVLYLVSGALVQALQPHQHEQQAQKQMDHGRDQFLRDHPCVSKSLED 60

QY 102 LIQIIVAINAGIIP---LGNYSNOISHWDLGSSFFAGTIVTTIGFCGNISPRTEGGKIF 158
Db 61 FIKLIVEALGGGANPETSWTNSNHNSSAWNLSGSAFFSGTITTTIGYCNIVLHTDAGRLF 120

QY 159 CIIVALLGIPLFGPLLAGVGDQGTIFGKGIKVEDTFIKWVSQTKIRIISTIFIILFG 218
Db 121 CIFVALVGIPLFGMLLAGVGDRLGSLRRGTHIEAIFLKHVPPCLVRSLSAVLFLIG 180

QY 219 CVLFVALPAIIPKHIEGWSALDAIYFVVITLTIGFDYVAGSDIEYLDYKPVVWFMI 278
Db 181 CLLFVLTPTFFVSYNESKLEAIYFVIVTLTTVGFVDYVPGDGTGQNSPAYQPLVWFMI 240

QY 279 LVGLAYFAVLVSMIGDWLRVSKTKYEEVGEPFAHAAEWANTVTA 323
Db 241 LFGLAYFASVLTITIGNWLRVSRRTAEWNGGLTAQAASWTGTVTA 285
```

Search completed: July 13, 2005, 08:44:29  
Job time : 96.9622 secs







```
Query Match 15.2%; Score 319; DB 2; Length 1001;
Best Local Similarity 28.4%; Pred. No. 1.1e-17;
Matches 89; Conservative 61; Mismatches 127; Indels 36; Gaps 10;

QY 50 IFLVVLYLIIGATVFKALQEPHE-----ISQRTIVIQKQFFISQHSVCVNSTELDELIQ 105
DB 9 LLIFYSYLMFGAIIYHIEHBKEISRAEQKQAIAINEYLLLEELGDKNTVTTQDEILQR 68

QY 106 IVAAINAGIIPLGNTSQISHWDLGSGFFAGVTTTIGFNGNISPRTEGKIFCIIYALL 165
DB 69 ISDYCDKPVLTPTDYDDTPTWTFYHAFPAFTVCSIVGVGNISPTTFAGRMIMIAYSVI 128

QY 166 GIPFLGELLAGVGQDLGTIFGKGIKVEDTFIKWNVS-----QTKIRIISTIFIILF-G 218
DB 129 GIPVNGILFAG-----LCEYEGRTFEAIYRYKYYKSDMHVYPPQGLITTVVIALIPG 184

QY 219 CVLPFVALPAIEKHIEGMSALDAIFVWVITLTITIGGDYVA-----GSGDIEYLD 268
DB 185 IALFLLPLPSWVTFYFENWPSYISLYSYVTTTIGFGDYVPTTFGANQPKFEGGWFVYQI 244

QY 269 FYKPVVFWFLVGLAYFAAALSMIGDMLRVISKK---TKEEVGEFRAHAAEWANTVTA 324
DB 245 FV--IWF--IFSLGYLWMTITRCLQ--SKLAYLEQQLSSNLKATQNRIMWSGVTKD 298

QY 325 FKETRRRLSVEIY 337
DB 299 VGYLRRLMN-ELY 310

RESULT 6
T23182
hypotheical protein K01D12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23182
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:Cross-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.4
A:Map position: 5
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 13.7%; Score 288; DB 2; Length 383;
Best Local Similarity 23.6%; Pred. No. 1.1e-15;
Matches 85; Conservative 80; Mismatches 127; Indels 68; Gaps 12;

QY 20 LPSSTKPTVLASRVESDITINNMKKT-VSTIFLVVLYLIIGATVFKALQEPHEISQRT 78
DB 16 LRANTLPSITRAKVGCGFARLRIYEENARFVLCIILIVLAFGAILFHWLEWENYDERI 75

QY 79 TI---VIQKTFISQHSVCVNSTELDELIQIVAAINAGIIPLGNTSQISHWDLGSGFF 135
DB 76 AIDNRWADYQVKYCKRKLNECFEENVRPISDQATSGLL-----NSRSPFHLGSLFF 129

QY 136 AGTVITTTIGFNGISPRTEGKIFCIIYALIG-----IPLFGFLAGVGQDLGTIFGKGIK 191
DB 130 SATVISTIGTSTPRTHLGRFTITIVGVGCTCCVLFFNLFL-----ERLVTGMSYLAS 185

QY 192 VEDTFIKWNVSQTKIRIISTII-----FILFG-CVLFV 223
DB 186 LRERKIRYRLKSGKNPKVTLILLNEDFNESSSCGGHMDNWRPSVYKVFILFPMCLVLI 245

QY 224 ALPAIFKHIEGMSALDAIFVWVITLTITIGFGDYVAGSDIEYL--DFYKPVVFWFILI 281
DB 246 TASAGIYSVVENWNYIDSLYFCFISPATIGFGDYVSNQDQVTRMSPDLYRFVNFCLLTIG 305

QY 282 LAYF-----AAVLSMIGDMLRVISKTKKEVEGFRAHAAEWANTVTAEFKTRRLSV 334
DB 306 ACFFYCLSVSSIVVRLQLNWM---IKMDVKV-EDRSPFLC-----FKKRRYVMTG 352

RESULT 7
T19860
hypotheical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 13.5%; Score 284.5; DB 2; Length 334;
Best Local Similarity 27.4%; Pred. No. 1.8e-15;
Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

QY 50 IFLVVLYLIIGATVFKALQEPHEISQRTIV---IQKTFISQHSVCVNSTELDELIQ 106
DB 14 LILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIRITDRLKHK-YNFSERDLHLFEA 67

QY 107 VAAINAGIIPLGNTSQISH-WDLGSGSFFAGVTTTIGFNGISPRTEGKIFCIIYALL 165
DB 68 IA-----IKSIPOAGYQWQFAGATVTTITVGVGHSAPSTNAGKLCFMIPLF 119

QY 166 GIPFLGFLAGVGQDLGTIFGKGIKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG 218
DB 120 GVPMLIMFQSIGERVNTFIAYSLHKFRDSLHQOQFTCLQEVTPTHLLMVSLTIGFVW-- 177

QY 219 CVLPFVALPAIEKHIEGMSALDAIFVWVITLTITIGFGDYV--AGGSDIEYLDYKPVVWF 276
DB 178 ----IVSGTYMFHTIEKNSIFDAYFYFCMITFTSTIGFDLVPLQQVNALQDQPLYVFATIM 233

QY 277 WILVGLAYFAAALSMIGDMLRVISKTKKEVEGFRAHAAEWANTVTAEFKTRRLSVEI 336
DB 234 FILGLAVESACVNL-----VLGFMASNADEVTA-----AQREPPSAIV 273

QY 337 YDKFORATSIKRKL 350
DB 274 LERFTNSLVDSQI 287

RESULT 8
T43361
probable potassium channel chain n2p20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43361
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-364 <WAN>
A:Cross-references: UNIPROT:O76790; EMBL:AF083646; PIDN:AAC32857.1

Query Match 13.5%; Score 284.5; DB 2; Length 364;
Best Local Similarity 27.4%; Pred. No. 2e-15;
```



Db 339 TTWATTGYGNIVPTPLGRACLVLFALGAPIALIITIGDLQKFLSECTIWLKWKRGKSA 339  
 QY 191 KVEDTTFKW-----NVSQTKIRIISTITIFILFGCV 220  
 Db 399 RLDSAMKRFRLGLEDSDLESASKNQDSSILDMQDEIDKSEVPVLMVFTHI-----L 452  
 QY 221 LFFVALPAIIFPKHIEGHSALDAIVFVITLTITIGFDYVAGSDIEYLDFFPKVWVFWILY 280  
 Db 453 LXTAFQGLIFSLIEDWSYMDAFYYSFISLTITIGFDIVPENHD-----YIAIMLIYLG 506  
 QY 281 GLIAYFAAVALSMIG-----DWLRVISKTK-----EEVGEPRAH 313  
 Db 507 GLSVTTMCDLGIQYIKHYFGRKFGQTDLLQYLKKRMLERRLANGQGEIILRKVH 566  
 QY 314 AAEWTANVTAEFKETRRRLSVEIYDK 339  
 Db 567 AVE-----KPEREQEQLOQKMEE 585

RESULT 13  
 T15584  
 hypothetical protein C24A3.6 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T15584  
 R:Favella, T.  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of *C. elegans* cosmid C24A3.  
 A:Reference number: Z16373  
 A:Accession: T15584  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-325 <PAV>  
 A:Cross-references: EMBL:U40424; NID:g1065542; PID:g1065543; PIDN:AAA81455.1; C:Genetics:  
 A:Gene: CBSP:C24A3.6  
 A:Introns: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match 12.8%; Score 269; DB 2; Length 325;  
 Best Local Similarity 25.1%; Pred. No. 3.1e-14;  
 Matches 86; Conservative 53; Mismatches 88; Indels 116; Gaps 11

QY 46 TWSTTF-----LVVLYLIIGATVPKALEQPHISQRTTIVIQKTFISQHSVCN 95  
 Db 10 TILTTFKTFKGLLPLILVAYTLGAWIFWMEIGENE-----REMLIEQK--- 56  
 QY 96 STELDELIIQIVNAIN-----AGIIPLGNTSNOIS 125  
 Db 57 --ERDELIRTYKINQIQKRRRLMTABEEYNRTAKVITTFQETLGIQVPA--DMDKDI 112  
 QY 126 HDWLGSFFPAGTVITITIGFNISPRTEGKIFCIIVALLGIPFGFLLAGVGDLQGTIF 185  
 Db 113 HWTFLGSIYCMVTYTTIGYGNIVPTGWGRFATILYAFIGIPLTVLSLY----CLGSLP 168  
 QY 186 KGXIAKVEDTFIKWNSVQTKIRIIS-----STRVVSXDLNSKISEADNIEEGTTAITPSAEKTENNDDDL 210  
 Db 169 AKGCKMLWRFFLK-----STRVVSXDLNSKISEADNIEEGTTAITPSAEKTENNDDDL 222  
 QY 211 ----TIFILFGCVLFVALPAIIFPKHIEGHSALDAIVFVITLTITIGFDYVAGSDIEYL 267  
 Db 223 LSFPSIGLLIITVIWIFCAVLTFLEEMDFGTSLYPTLISFTITIGFDILP--SDVDFM 280  
 QY 268 DFVKPVPWFILVGLAYFAAVALSMIGDWLRVIS-----KKTKE 305  
 Db 281 ----PIVGVLIIIGLSLVSTMVLIQQQIEALASVRRKKKKK 319

RESULT 14  
 T24265  
 hypothetical protein T01B4.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T24265

C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T24265

R.Wilkinson, J.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19866  
A:Accession: T24265  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-522 <WIL>  
A:Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:FL1  
A:Experimental source: clone T01B4  
C:Genetics:  
A:Gene: CESP:T01B4.1  
A:Map position: X  
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.7%; Score 266; DB 2; Length 522;  
Best Local Similarity 23.1%; Pred. No. 9.7e-14;  
Matches 99; Conservative 64; Mismatches 134; Indels 134; Gaps 15;  
QY 50 IFLVVLYLIIGATVFKALEQPH-----ISQRTTIVIQKTFIISOHSCVNSTE 98  
DB 41 LILILGACLGGMFOALEYDQOOLEAEAKRVLSSLLAVNLLHLLKQMGQSGNE 100  
QY 99 LDELIIQIVAAINAGIIPLGNTS-NQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKI 157  
DB 101 -----KRCLELITKTFIQSDEREGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGR 155  
QY 158 FCIIYALGIPFGFLLAGVGD-----OLGTIFGK 188  
DB 156 ATIIYGMIGIPLMLFVLKFGELCVKAKKIQFNVOQCKKCFGRKQKRASSLASITSKE 215  
QY 189 IAKV-----EDTF--IKWNSQTKIRIISTIIIFILFGCVLFPALPAIFKHIEGWS 237  
DB 216 MLEVFVEPDEKDTTTLRWG-----LLVIVLFLVCSFVSWFNWD 260  
QY 238 ALDAIFYFVITLTITGFGDYVAGSDIEYLPKPVVWFIL--VGLAYFAAVLSMIGD- 294  
DB 261 FLTAIFYFFVSLSITGFGDIVP-----DHPRTACALFVLYFGLFALFAMVYAILQER 312  
QY 295 -----W-LRVISKTKKEVEGEFRAHAAEWANVT----- 322  
DB 313 VENQYMWALELTDQYQEKLDQMDYDEDEKADKNDMHFSKKEPVGRPRILLQDLLRGPD 372  
QY 323 AEFKETRRLS-----VEIYDKFORATSIKKLSAEL-----AGNHQELTPCRRTLS 370  
DB 373 LKISGRSSDASSVITEASDETRHFKVGRAILLAEPAPDERASNHGTQNSCT---- 428  
QY 371 VNLHITNERD 379  
DB 429 ---VSNEHD 434

RESULT 15  
T21118  
hypothetical protein F19D8.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21118  
R:Swinsburne, J.; Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19377  
A:Accession: T21118  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-452 <WIL>  
A:Cross-references: UNIPROT:Q93531; EMBL:Z78541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:FL1  
A:Experimental source: clone F19D8  
C:Genetics:  
A:Gene: CESP:F19D8.1  
A:Map position: X  
A:Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3  
Query Match 12.5%; Score 262; DB 2; Length 452;  
Best Local Similarity 28.5%; Pred. No. 1.7e-13;

Matches 81; Conservative 50; Mismatches 121; Indels 32; Gaps 7;  
QY 42 MKWKTVSTI-----FLVVVLYLIIGATVFKALE-----OPHEISQRTTIVIQKTFIS 89  
DB 36 MKFRNVLRIALGHLALYCFVVCYVFAGAWVPHQLEGENETELHDKQREYAMNLKKDVIK 95  
QY 90 QHSCVNSTELDELIIQIVAAINAGIIPLGN-----TSNQISHWDLGSSFFPAGTIVTT 142  
DB 96 LATTENVAEINEHURMFURNISNLHISLDNLIINEPTQIIVPKRWTFFSSVLFSTILT 155  
QY 143 IGFGNISPRTEGGKIFCIIYALGIPFGFLLAGVGDQGLTIFGKGIKAVEDTTFIKWNS 202  
DB 156 IGYGNVTPHTQCKVFLMIYGAFGLPLITLITADLGRFSKTAINALVQKSKRELKQSD 215  
QY 203 QTKIRIISTI---IFILFGCVLFPALPAIFKHIEGW-----SALDAIFYFVITLTITGFG 255  
DB 216 EHLREIAEVSPLYDLVLLVAGLFVVFVTAIGSAVPLMENQLTYPDSVYFSYMSLTITGLG 275  
QY 256 DYVAGGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVI 299  
DB 276 DIVP-----RRMDFLLPTL-IYITIGLWLTALVEQLADVERLV 313

Search completed: July 13, 2005, 08:45:40  
Job time : 24.6316 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 90.2442 Seconds  
(without alignments)  
1759.475 Million cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100

Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNLTPHCAGEIAVNIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pdb.pdb.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pdb.pdb.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pdb.pdb.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pdb.pdb.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pdb.pdb.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pdb.pdb.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pdb.pdb.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pdb.pdb.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pdb.pdb.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pdb.pdb.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pdb.pdb.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pdb.pdb.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pdb.pdb.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pdb.pdb.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pdb.pdb.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pdb.pdb.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pdb.pdb.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pdb.pdb.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pdb.pdb.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pdb.pdb.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pdb.pdb.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pdb.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2100	100.0	411	11	US-09-892-360-18
2	2095	99.8	411	9	US-09-828-746-2
3	2095	99.8	411	14	US-10-121-746-83
4	2095	99.8	411	16	US-10-745-210-2
5	2095	99.8	411	16	US-10-349-528-31
6	2095	99.8	411	17	US-10-976-644-83
7	2095	99.8	411	17	US-10-976-647-83
8	2089	99.5	422	16	US-10-349-528-20
9	2082	98.2	426	8	US-08-816-011-45
10	2062	98.2	426	17	US-10-870-492-45
11	2058	98.0	426	17	US-10-870-492-57

12	2057	98.0	426	17	US-10-870-492-58	Sequence 58, Appl
13	2054	97.8	426	17	US-10-870-492-60	Sequence 60, Appl
14	2053	97.8	426	17	US-10-870-492-59	Sequence 59, Appl
15	2035	96.9	411	9	US-09-828-746-6	Sequence 6, Appli
16	1824	86.9	370	9	US-09-939-484-8	Sequence 8, Appli
17	1824	86.9	370	9	US-09-939-483-8	Sequence 8, Appli
18	1249	59.5	538	9	US-09-729-920-5	Sequence 5, Appli
19	1249	59.5	538	16	US-10-887-932-5	Sequence 5, Appli
20	1243	59.2	526	9	US-09-729-920-4	Sequence 4, Appli
21	1243	59.2	526	16	US-10-887-932-4	Sequence 4, Appli
22	1243	59.2	538	11	US-09-892-360-2	Sequence 2, Appli
23	1243	59.2	538	18	US-10-923-035-46	Sequence 2, Appli
24	1243	59.2	543	9	US-09-729-920-2	Sequence 2, Appli
25	1243	59.2	543	10	US-09-852-386-73	Sequence 73, Appl
26	1243	59.2	543	14	US-10-332-175-2	Sequence 2, Appli
27	1243	59.2	543	15	US-10-262-511-106	Sequence 106, App
28	1243	59.2	543	16	US-10-887-932-2	Sequence 2, Appli
29	1215.5	57.9	724	15	US-10-332-447-10	Sequence 10, Appl
30	803	38.2	392	9	US-09-747-835A-55	Sequence 55, Appl
31	803	38.2	392	15	US-10-312-312-55	Sequence 2, Appli
32	803	38.2	393	14	US-10-243-035-2	Sequence 2, Appli
33	803	38.2	419	9	US-09-828-035-2	Sequence 2, Appli
34	803	38.2	419	14	US-10-345-680-44	Sequence 44, Appl
35	803	38.2	419	14	US-10-146-733-29	Sequence 29, Appl
36	803	38.2	419	15	US-10-352-684A-8	Sequence 8, Appli
37	803	38.2	419	15	US-10-391-399-19	Sequence 19, Appl
38	803	38.2	419	16	US-10-768-158-12	Sequence 12, Appl
39	803	38.2	481	18	US-10-852-707-65	Sequence 65, Appl
40	803	38.2	822	18	US-10-852-707-64	Sequence 64, Appl
41	803	38.2	1314	9	US-09-747-835A-29	Sequence 29, Appl
42	803	38.2	1314	15	US-10-312-312-29	Sequence 29, Appl
43	776.5	37.0	398	11	US-09-892-360-19	Sequence 19, Appl
44	732	34.9	924	18	US-10-852-707-66	Sequence 66, Appl
45	732	34.9	1125	18	US-10-852-707-60	Sequence 60, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-892-360-18  
; Sequence 18, Application US/09892360  
; Publication No. US20040101833A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: ROMERY, GEORGES  
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
; FILE REFERENCE: RILUZOLE  
; FILE REFERENCE: 1256-R-00  
; CURRENT APPLICATION NUMBER: US/09/892,360  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 60/214,559  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-892-360-18

Query Match 100.0%; Score 2100; DB 11; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.7e-188;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTFVLVWLYLI 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTFVLVWLYLI 60  
QY 61 GATVFKALEQPHSEISORTTIVIKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 120

Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 120  
Qy 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Qy 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Qy 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360  
Qy 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411  
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411

## RESULT 2

US-09-828-746-2  
; Sequence 2, Application US/09828746  
; Patent No. US20020028485A1  
; GENERAL INFORMATION:  
; APPLICANT: Helen Jane Meadows  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30031-D1  
; CURRENT APPLICATION NUMBER: US/09/828,746  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 09/236,080  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: EP 98300570.3  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: UK 9822135.1  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-828-746-2

Query Match 99.8%; Score 2095; DB 9; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.le-187;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Qy 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 120  
Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 120  
Qy 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Qy 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Qy 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360

Db 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360  
Qy 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411  
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411

## RESULT 3

US-10-121-746-83  
; Sequence 83, Application US/10121746  
; Publication No. US20030036648A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/121,746  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US/09/336,643A  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-10-121-746-83

Query Match 99.8%; Score 2095; DB 14; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.le-187;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Qy 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 120  
Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 120  
Qy 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180  
Qy 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDFFIKWNSQTKIRIISTITIFILFGCVLFVALPALIIFKHIEGWSALD 240  
Qy 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVMFWILVGLAYFAAULSMIGDMLRVIS 300  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTAVTAEPKTRRRLSVEIYDKFORATSIKRLKLSAELAGNHQ 360  
Qy 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411  
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411  
RESULT 4  
US-10-745-210-2



```
; Sequence 2, Application US/10745210
; Publication No. US2004014385A1
; GENERAL INFORMATION:
; APPLICANT: TONONI, Giulio
; APPLICANT: CIRELLI, Chiara
; FILE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
; FILE REFERENCE: 054030-0044
; CURRENT APPLICATION NUMBER: US/10/745,210
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,201
; PRIOR FILING DATE: 2001-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-745-210-2

Query Match      99.8%; Score 2095; DB 16; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQVAAINAGIIPLGNT 120
DB 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQVAAINAGIIPLGNT 120
QY 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIAKVEDTEIKNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
DB 181 LGTIFGKGIAKVEDTEIKNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360
DB 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360
QY 361 ELTPCRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411
DB 361 ELTPCRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411

RESULT 5
US-10-349-528-31
; Sequence 31, Application US/10349528
; Publication No. US2004025366A1
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; FILE REFERENCE: D0210
; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-10-349-528-31
```

```
Query Match      99.8%; Score 2095; DB 16; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQVAAINAGIIPLGNT 120
DB 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQVAAINAGIIPLGNT 120
QY 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIAKVEDTEIKNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
DB 181 LGTIFGKGIAKVEDTEIKNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360
DB 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360
QY 361 ELTPCRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411
DB 361 ELTPCRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411

RESULT 6
US-10-976-644-83
; Sequence 83, Application US/10976644
; Publication No. US20050112662A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,644
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
; US-10-976-644-83

Query Match      99.8%; Score 2095; DB 17; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSPSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQVAAINAGIIPLGNT 120
```

Db 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 120  
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 180  
Db 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 180  
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
QY 241 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 300  
Db 241 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 300  
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 360  
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411  
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411

## RESULT 7

US-10-976-647-83  
; Sequence 83, Application US/10976647  
; Publication No. US20050112863A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: Novel Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/10/976,647  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/336,643  
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-10-976-647-83

Query Match 99.8%; Score 2095; DB 17; Length 411;  
Best Local Similarity 99.8%; Pred. No. 1.1e-187;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTSTIFLVVLYLII 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTSTIFLVVLYLII 60  
QY 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 120  
Db 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 120  
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 180  
Db 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 180  
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240

QY 241 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 300  
Db 241 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 300  
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 360  
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411  
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411

## RESULT 8

US-10-349-528-20  
; Sequence 20, Application US/10349528  
; Publication No. US20040253668A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMANATHAN, Chandra  
; APPLICANT: GOPAL, Shuba  
; APPLICANT: MINTIER, Gabe  
; APPLICANT: FEDER, John  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF  
; FILE REFERENCE: D0210  
; CURRENT APPLICATION NUMBER: US/10/349,528  
; CURRENT FILING DATE: 2003-01-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-10-349-528-20

Query Match 99.5%; Score 2089; DB 16; Length 422;  
Best Local Similarity 99.3%; Pred. No. 4.1e-187;  
Matches 408; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTSTIFLVVLYLII 60  
Db 12 LAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKWKTSTIFLVVLYLII 71  
QY 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 120  
Db 72 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTELDELIQIVAAINAGIPLGNT 131  
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 180  
Db 132 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQD 191  
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 192 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 251  
QY 241 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 300  
Db 252 AIYFVVTITLTITGFGDYVAGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDWLRVIS 311  
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 360  
Db 312 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVBIYDKFQRTATSIKRKLSAELAGNHQ 371  
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411  
Db 372 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 422

## RESULT 9

US-08-816-011-45  
; Sequence 45, Application US/08816011  
; Publication No. US20030165806A1

GENERAL INFORMATION:  
APPLICANT: Price, Laura A.  
APPLICANT: Pausch, Mark H.  
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,011  
FILING DATE: 11-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthews, Gale F.  
REGISTRATION NUMBER: 32,269  
REFERENCE/DOCKET NUMBER: 32,421-C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2134  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-816-011-45

Query Match 98.2%; Score 2062; DB 8; Length 426;  
Best Local Similarity 98.5%; Pred. No. 1.4e-184;  
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75  
QY 61 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIIQIIVAAINAGIIPLGNT 120  
DB 76 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIIQIIVAAINAGIIPLGNT 135  
QY 121 SNQISHWDLGSSFFFAAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLLAGVGQ 180  
DB 136 SNQISHWDLGSSFFFAAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLLAGVGQ 195  
QY 181 LGTIFGKGIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
DB 196 LGTIFGKGIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255  
QY 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 300  
DB 256 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 315  
QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360  
DB 316 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375  
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411  
DB 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 426

## RESULT 10

US-10-870-492-45

; Sequence 45, Application US/10870492

Publication No. US20050032165A1  
GENERAL INFORMATION:  
APPLICANT: PAUSCH, MARK H.  
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
TITLE OF INVENTION: AND METHODS OF USING SAME  
FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
CURRENT APPLICATION NUMBER: US/10/870,492  
CURRENT FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: US/09/503,849  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/816,011  
PRIOR FILING DATE: 1997-03-11  
PRIOR APPLICATION NUMBER: PCT/US95/14364  
PRIOR FILING DATE: 1995-10-25  
PRIOR APPLICATION NUMBER: 07/332,312  
PRIOR FILING DATE: 1994-10-31  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 45  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-870-492-45

Query Match 98.2%; Score 2062; DB 17; Length 426;  
Best Local Similarity 98.5%; Pred. No. 1.4e-184;  
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75  
QY 61 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIIQIIVAAINAGIIPLGNT 120  
DB 76 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIIQIIVAAINAGIIPLGNT 135  
QY 121 SNQISHWDLGSSFFFAAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLLAGVGQ 180  
DB 136 SNQISHWDLGSSFFFAAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLLAGVGQ 195  
QY 181 LGTIFGKGIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
DB 196 LGTIFGKGIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255  
QY 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 300  
DB 256 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 315  
QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360  
DB 316 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375  
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411  
DB 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 426

## RESULT 11

US-10-870-492-57

; Sequence 57, Application US/10870492

; Publication No. US20050032165A1

; GENERAL INFORMATION:

; APPLICANT: PAUSCH, MARK H.

; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

; FILE REFERENCE: 01142.0114 SEQUENCE LISTING

; CURRENT APPLICATION NUMBER: US/10/870,492

; CURRENT FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: US/09/503,849

; PRIOR FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 08/816,011

; PRIOR FILING DATE: 1997-03-11

; PRIOR APPLICATION NUMBER: PCT/US95/14364

```
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-57

Query Match          98.0%; Score 2058; DB 17; Length 426;
Best Local Similarity 98.3%; Pred. No. 3.4e-184;
Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 60
   :|||||
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 75
   :|||||

QY 61 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 120
   :|||||
Db 76 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 135
   :|||||

QY 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 180
   :|||||
Db 136 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 195
   :|||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD 240
   :|||||
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD 255
   :|||||

QY 241 AIYFVVITLTTTIGFDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
   :|||||
Db 256 AIYFVVITLTTTIGFDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGRLVRVIS 315
   :|||||

QY 301 KKTKEEVGEFRAHAAEWANTVTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
   :|||||
Db 316 KKTKEEVGEFRAHAAEWANTVTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
   :|||||

QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYINGLTPHCAGEIAVIENIK 411
   :|||||
Db 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYINGLTPHCAGEIAVIENIK 426
   :|||||

RESULT 12
US-10-870-492-58
; Sequence 58, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-58

Query Match          98.0%; Score 2057; DB 17; Length 426;
Best Local Similarity 98.3%; Pred. No. 4.2e-184;
Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 60
   :|||||
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 75
   :|||||

QY 61 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 120
   :|||||
Db 76 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 135
   :|||||

QY 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 180
   :|||||
Db 136 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 195
   :|||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD 240
   :|||||
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD 255
   :|||||

QY 241 AIYFVVITLTTTIGFDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
   :|||||
Db 256 AIYFVVITLTTTIGFDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGRLVRVIS 315
   :|||||

QY 301 KKTKEEVGEFRAHAAEWANTVTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
   :|||||
Db 316 KKTKEEVGEFRAHAAEWANTVTAEFKTRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
   :|||||

QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYINGLTPHCAGEIAVIENIK 411
   :|||||
Db 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYINGLTPHCAGEIAVIENIK 426
   :|||||

RESULT 13
US-10-870-492-60
; Sequence 60, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-60

Query Match          97.8%; Score 2054; DB 17; Length 426;
Best Local Similarity 98.3%; Pred. No. 8e-184;
Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 60
   :|||||
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 75
   :|||||

QY 61 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 120
   :|||||
Db 76 GATVPKALEQPEHISORTTIVIQKOTFISQHSVCVNSTELDELIQOIVAAINAGIIPLGNT 135
   :|||||

QY 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 180
   :|||||
Db 136 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQD 195
   :|||||
```

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255  
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300  
Db 256 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGRLVRVIS 315  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 360  
Db 316 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 375  
Qy 361 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 411  
Db 376 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 426  
RESULT 14  
US-10-870-492-59  
; Sequence 59, Application US/10870492  
; Publication No. US20050032165A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUSCH, MARK H.  
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/10/870,492  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: US/09/503,849  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/816,011  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR APPLICATION NUMBER: PCT/US95/14364  
; PRIOR FILING DATE: 1995-10-25  
; PRIOR APPLICATION NUMBER: 07/332,312  
; PRIOR FILING DATE: 1994-10-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-870-492-59

Query Match 97.8%; Score 2053; DB 17; Length 426;  
Best Local Similarity 98.1%; Pred. No. 9.9e-184;  
Matches 403; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Db 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75  
Qy 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQQIVAAINAGIIPLGNT 120  
Db 76 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQQIVAAINAGIIPLGNT 135  
Qy 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGILPLFGFLLAGVGDQ 180  
Db 136 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGILPLFGFLLAGVGDQ 195  
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255  
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300  
Db 256 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGRLVRVIS 315  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 360  
Db 316 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 375

Qy 361 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 411  
Db 376 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 426  
RESULT 15  
US-09-828-746-6  
; Sequence 6, Application US/09828746  
; Patent No. US20020028485A1  
; GENERAL INFORMATION:  
; APPLICANT: Helen Jane Meadows  
; APPLICANT: Conrad Gerald Chapman  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30031-D1  
; CURRENT APPLICATION NUMBER: US/09/828,746  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 09/236,080  
; PRIOR FILING DATE: 1999-01-25  
; PRIOR APPLICATION NUMBER: EP 98300570.3  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: UK 9822135.1  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-828-746-6

Query Match 96.9%; Score 2035; DB 9; Length 411;  
Best Local Similarity 95.9%; Pred. No. 4.6e-182;  
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
Qy 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQQIVAAINAGIIPLGNT 120  
Db 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQQIVAAINAGIIPLGNS 120  
Qy 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGILPLFGFLLAGVGDQ 180  
Db 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGILPLFGFLLAGVGDQ 180  
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240  
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300  
Db 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300  
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 360  
Db 301 KKTKEEVGEFRAHAAEWNTAVTAEFKETRRLRSVEIYDKFORATSIRKRLSAELAGNHQ 360  
Qy 361 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 411  
Db 361 ELTPCRTLSTVNLHNTNDRDVLPLLLKTESIYLNGLTPHCGAEEIAVIENIK 411

Search completed: July 13, 2005, 09:07:00  
Job time : 92.2442 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds  
(without alignments)  
1163.760 Million cell updates/sec

Title: US-09-503-089A-2  
Perfect score: 2100  
Sequence: 1 MAAPDLLDPKSAQNSKPL.....LNLTPHCAGEBIAVNIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	3	US-09-236-080-2
2	2095	99.8	411	3	US-09-336-643A-83
3	2035	96.9	411	3	US-09-236-080-6
4	1824	86.9	370	3	US-09-144-914-8
5	1243	59.2	538	4	US-09-949-016-7001
6	1243	59.2	558	4	US-09-949-016-7368
7	803	38.2	393	4	US-09-432-470-2
8	803	38.2	393	4	US-09-432-470-4
9	803	38.2	419	4	US-09-949-016-6913
10	803	38.2	440	4	US-09-949-016-7809
11	547	26.0	107	3	US-09-236-080-4
12	427	20.3	499	4	US-09-561-763-2
13	427	20.3	499	4	US-09-431-367B-2
14	391	18.6	332	4	US-09-561-763-5
15	391	18.6	332	4	US-09-431-367B-5
16	382	18.1	361	4	US-09-362-842-14
17	379.5	18.2	336	3	US-08-749-816-2
18	379.5	18.1	336	3	US-09-144-914-2
19	363	17.3	394	3	US-09-144-914-4
20	349.5	16.6	388	4	US-09-949-016-7631
21	348	16.6	313	3	US-09-336-643A-81
22	348	16.6	313	4	US-09-561-763-8
23	348	16.6	313	4	US-09-431-367B-8
24	337	16.0	405	3	US-09-144-914-5
25	309.5	14.7	408	4	US-09-362-842-12
26	291.5	13.9	618	1	US-08-332-312-2
27	284	13.5	257	4	US-09-949-016-6654

28	284	13.5	273	4	US-09-949-016-7794	Sequence 7794, Ap
29	261.5	12.5	395	4	US-09-362-842-6	Sequence 6, Appli
30	221.5	10.5	730	4	US-09-362-842-4	Sequence 4, Appli
31	221.5	10.5	741	4	US-09-362-842-67	Sequence 67, Appl
32	221.5	10.5	741	4	US-09-270-767-45442	Sequence 45442, A
33	221	10.5	336	1	US-08-332-312-4	Sequence 4, Appli
34	209	10.0	995	4	US-09-362-842-2	Sequence 2, Appli
35	205	9.8	401	4	US-09-561-763-11	Sequence 11, Appl
36	205	9.8	401	4	US-09-431-367B-11	Sequence 11, Appl
37	179	8.5	383	3	US-08-749-816-4	Sequence 4, Appli
38	179	8.5	383	3	US-09-144-914-7	Sequence 7, Appli
39	166.5	7.9	1153	4	US-09-362-842-8	Sequence 8, Appli
40	160.5	7.6	347	3	US-08-749-816-3	Sequence 3, Appli
41	160.5	7.6	347	3	US-09-144-914-6	Sequence 6, Appli
42	153.5	7.3	197	3	US-09-336-643A-16	Sequence 16, Appl
43	140	6.7	146	4	US-09-362-842-69	Sequence 69, Appl
44	140	6.7	146	4	US-09-270-767-31685	Sequence 31685, A
45	130.5	6.2	391	4	US-09-543-681A-7029	Sequence 7029, Ap

ALIGNMENTS

RESULT 1

US-09-236-080-2

; Sequence 2, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match	99.8%	Score	2095;	DB	3;	Length	411;
Best Local Similarity	99.8%	Pred. No.	4.7e-205;				
Matches	410;	Conservative	1;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTFIWVLYLII	60				
Db	1	MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTFIWVLYLII	60				
Qy	61	GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIIPLGNT	120				
Db	61	GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIIPLGNT	120				
Qy	121	SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFGLLAGVGQD	180				
Db	121	SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFGLLAGVGQD	180				
Qy	181	LGTIFGKGIKAVEDFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD	240				
Db	181	LGTIFGKGIKAVEDFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD	240				
Qy	241	AIYFVVIITLTITGFDGYVAGGSDIEYLFQKPVWFWILVGLAYFAAVLSMIGDMLRVIS	300				
Db	241	AIYFVVIITLTITGFDGYVAGGSDIEYLFQKPVWFWILVGLAYFAAVLSMIGDMLRVIS	300				
Qy	301	KKTKEVEGFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKRLKSLAELAGNNHQ	360				
Db	301	KKTKEVEGFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSIKRLKSLAELAGNNHQ	360				
Qy	361	ELTPCRRLTSVNNHLTNERDVLPLKTESIYINGLTPHCAGEBIAVNIK 411					
Db	361	ELTPCRRLTSVNNHLTNERDVLPLKTESIYINGLTPHCAGEBIAVNIK 411					

```
RESULT 2
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
; US-09-336-643A-83

Query Match          99.8%; Score 2095; DB 3; Length 411;
Best Local Similarity 99.8%; Pred. No. 4.7e-205;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDITINNWKKTSTFIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDITINNWKKTSTFIFLVVLYLII 60
QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
QY 121 SNOISHWDLGSSFFPAGTIVITIGFNGISPRTEGKIFCIIYALLGIPFGFLLAGVGQ 180
Db 121 SNOISHWDLGSSFFPAGTIVITIGFNGISPRTEGKIFCIIYALLGIPFGFLLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
QY 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGFRAHAAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
Db 301 KKTKEEVGFRAHAAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
QY 361 ELTPCRRRLTSVNHLTSDRDLVPLPKTESIYNGLTTPHCAGEIAVIENIK 411
Db 361 ELTPCRRRLTSVNHLTSDRDLVPLPKTESIYNGLTTPHCAGEIAVIENIK 411

RESULT 3
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080

Query Match          86.9%; Score 1824; DB 3; Length 370;
Best Local Similarity 86.9%; Pred. No. 6.2e-199;
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDITINNWKKTSTFIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDITINNWKKTSTFIFLVVLYLII 60
QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
QY 121 SNOISHWDLGSSFFPAGTIVITIGFNGISPRTEGKIFCIIYALLGIPFGFLLAGVGQ 180
Db 121 SNOISHWDLGSSFFPAGTIVITIGFNGISPRTEGKIFCIIYALLGIPFGFLLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
QY 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVTITTTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGFRAHAAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
Db 301 KKTKEEVGFRAHAAEWNTANTAEFKETRRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
QY 361 ELTPCRRRLTSVNHLTSDRDLVPLPKTESIYNGLTTPHCAGEIAVIENIK 411
Db 361 ELTPCRRRLTSVNHLTSDRDLVPLPKTESIYNGLTTPHCAGEIAVIENIK 411

RESULT 4
US-09-144-914-8
; Sequence 8, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Pink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
; US-09-144-914-8

Query Match          86.9%; Score 1824; DB 3; Length 370;
```



Best Local Similarity 96.5%; Pred. No. 1.8e-177;  
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60  
DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60

QY 61 GATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIQQIIVAAINAGIIPLGNT 120  
DB 61 GAAVFKALEQPEHISQRTTIVIQKTFIAQHACVNSTELDELIQQIIVAAINAGIIPLGNS 120

QY 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGLLAGVQDQ 180  
DB 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPFGLLAGVQDQ 180

QY 181 LGTIFGKGIAKVEDTIFKNVSTQKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240  
DB 181 LGTIFGKGIAKVEDTIFKNVSTQKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240

QY 241 AIYFVVVITLTIGFDYVAGGSDIEYLDYKPVVWFWLVLGLAYFAAVLSMIGDMLRVIS 300  
DB 241 AIYFVVVITLTIGFDYVAGGSDIEYLDYKPVVWFWLVLGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTAETAEKTRRRRLSVIYDKFORATSIRKLSAELAGNHQ 360  
DB 301 KKTKEEVGFRAHAAEWNTAETAEKTRRRRLSVIYDKFORATSIRKLSAELAGNHQ 360

QY 361 ELTPCRR 368  
DB 361 ELTPCRR 368

RESULT 5  
US-09-949-016-7001  
; Sequence 7001, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7001  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7001

Query Match 59.2%; Score 1243; DB 4; Length 538;  
Best Local Similarity 62.7%; Pred. No. 6.1e-118;  
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNPKRLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50  
DB 17 AAPVCQPKSATNGOPPAPPTPTPLRLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75

QY 51 FLVVVLYLIGATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIQQIIVAAI 110  
DB 76 FVVVVVYLVTLGVLFPALQPESSQKNTIALEKAEFLRDHVCVSPQELTIQHALDAD 135

QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPF 170  
DB 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAIIFGIPF 195

QY 171 GFLLAGVGDQLTIFGKGIAKVEDTIFKNVSTQKIRIISTIFILFGCVLFVALPAIIF 230  
DB 196 GFLLAGVGDQLTIFGKSIAKVEKVPKQVSTQKIRIVISTILFILAGCIVFTVPAVIF 255

QY 231 KHIEGWSALDAIYFVVTITLTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289  
DB 256 KYIEGWTALIESIYFVVVTLTITVGFDVAGGNAGINREWKYKPLVWFWLVLGLAYFAAVL 315

QY 290 SMIGDMLRVISKKTKEEVGFRAHAAEWNTAETAEKTRRRRLSVIYDKFORATSIRK 349  
DB 316 SMIGDMLRVLSKKTKEEVGEIKAHAAEWKANTAEFRETRRRRLSVIYDKFORATSIRK 373

QY 350 LSAELAGNHQBELTPCRRLTSVNLHNTNRDVLPP 383  
DB 374 -SME-----RRRLGLDQRAHSLDMLSP 394

RESULT 6  
US-09-949-016-7368  
; Sequence 7368, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7368  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7368

Query Match 59.2%; Score 1243; DB 4; Length 558;  
Best Local Similarity 62.7%; Pred. No. 6.4e-118;  
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNPKRLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50  
DB 37 AAPVCQPKSATNGOPPAPPTPTPLRLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 95

QY 51 FLVVVLYLIGATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIQQIIVAAI 110  
DB 96 FVVVVVYLVTLGVLFPALQPESSQKNTIALEKAEFLRDHVCVSPQELTIQHALDAD 155

QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIPF 170  
DB 156 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAIIFGIPF 215

QY 171 GFLLAGVGDQLTIFGKGIAKVEDTIFKNVSTQKIRIISTIFILFGCVLFVALPAIIF 230  
DB 216 GFLLAGVGDQLTIFGKSIAKVEKVPKQVSTQKIRIVISTILFILAGCIVFTVPAVIF 275

QY 231 KHIEGWSALDAIYFVVTITLTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289  
DB 276 KYIEGWTALIESIYFVVVTLTITVGFDVAGGNAGINREWKYKPLVWFWLVLGLAYFAAVL 335

QY 290 SMIGDMLRVISKKTKEEVGFRAHAAEWNTAETAEKTRRRRLSVIYDKFORATSIRK 349  
DB 336 SMIGDMLRVLSKKTKEEVGEIKAHAAEWKANTAEFRETRRRRLSVIYDKFORATSIRK 393

QY 350 LSAELAGNHQBELTPCRRLTSVNLHNTNRDVLPP 383  
DB 394 -SME-----RRRLGLDQRAHSLDMLSP 414

```
RESULT 7
US-09-432-470-2
; Query Match 38.2%; Score 803; DB 4; Length 393;
; Best Local Similarity 51.1%; Pred. No. 3e-73;
; Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
; SEQUENCE: US/09432470
; PATENT NO. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; EARLIER FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-2
```

```
Query Match 38.2%; Score 803; DB 4; Length 393;
Best Local Similarity 51.1%; Pred. No. 3e-73;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
;
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913
```

```
RESULT 8
US-09-432-470-4
; Query Match 38.2%; Score 803; DB 4; Length 419;
; Best Local Similarity 51.1%; Pred. No. 3.3e-73;
; Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
; SEQUENCE: US/09432470
; PATENT NO. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; EARLIER FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-4
```

```
Query Match 38.2%; Score 803; DB 4; Length 393;
Best Local Similarity 51.1%; Pred. No. 3e-73;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
;
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913
```

```
RESULT 9
US-09-949-016-6913
; Sequence 6913, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913
```

```
Query Match 38.2%; Score 803; DB 4; Length 419;
Best Local Similarity 51.1%; Pred. No. 3.3e-73;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
;
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913
```

RESULT 10  
US-09-949-016-7809  
; Sequence 7809, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7809  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7809

Query Match 38.2%; Score 803; DB 4; Length 440;  
Best Local Similarity 51.1%; Pred. No. 3.5e-73;  
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;  
QY 42 MKWKTSTPLVVLVYLITGATVFKALQEPHEISQRTTIVIQKTFISQHSVCNVELDE 101  
DB 48 MRSTLLALLALLVLSGALVFRALQEPHEQQAQRELGVREKFLRAHPCVSDQELGL 107  
QY 102 LQCOIVAINAGIPLGNTSNQISH--WDLGSSFFAGTIVITIGFNGNISPRTEGKIFC 159  
DB 108 LIKEVADAGGGADPTNSTSSSHSANDLGSAPFFSGTIITIGYGNVALRTDAGRLFC 167  
QY 160 IYALIGLIPFGFLAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGC 219  
DB 168 IFYALVGIPLFGILLAGVDRGLGSSLRHGIGHIEAFLKHWVPELVRVLAMFLILGC 227  
QY 220 VLFVALPAIIFKHIEGWSALDAIFYVITLTITIGFDGYVAGGSDIEYLDYKPVVWFIL 279  
DB 228 LLFVLTPTEVFCMEDWSKLEAIYFVITLTITIGFDGYVAGADPRQDSPAYQPLVWFIL 287  
QY 280 VGLAYPAAVLSMGDLWLRVSKKTEKEVEGFRAHAAEWNTANVTA 323  
DB 288 LGLAYPASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 331

RESULT 11  
US-09-236-080-4  
; Sequence 4, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236,080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-236-080-4

Query Match 26.0%; Score 547; DB 3; Length 107;  
Best Local Similarity 98.1%; Pred. No. 5.6e-48;

Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 119 NTSNQISHWDLGSSFFAGTIVITIGFNGNISPRTEGKIFCIIYALLGIPFLGVLAVG 178  
DB 1 NSSNQSHWDLGSSFFAGTIVITIGFNGNISPRTEGKIFCIIYALLGIPFLGVLAVG 60  
QY 179 DQLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGCVLFAVAL 225  
DB 61 DQLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGCVLFAVAL 107  
RESULT 12  
US-09-561-763-2  
; Sequence 2, Application US/09561763  
; Patent No. 6664373  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Roy A. J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; CURRENT FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999  
; PRIOR APPLICATION NUMBER: US 09/259,951  
; PRIOR FILING DATE: 01-03-1999  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-561-763-2

Query Match 20.3%; Score 427; DB 4; Length 499;  
Best Local Similarity 31.1%; Pred. No. 1e-34;  
Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;  
QY 54 VVLYLIIGATVPKALEQPHEISQRTTIVIQKTFISQHSVCNVELDELIQIIVAAINAG 113  
DB 12 IIFLYAIGAAIPEVLEEPHWEAKKNYYTKLHLKPEPCLGQEGDLKILEVVSDAAGQ 71  
QY 114 IPLGNTSNQISHWDLGSSFFAGTIVITIGFNGNISPRTEGKIFCIIYALLGIPFLGFL 173  
DB 72 VAITGNQT--FNNWNPAMIFAATVITIGYGNVAPKTPAGRLFCVYGLGVPPL---C 126  
QY 174 LAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGCVLFAVALPAIIFKHI 233  
DB 127 LTWI-SALGKFFGGRAKRLGQLTKRGVSLRKAQITCTVIFVWGLVHLVIPPFFVMT 185  
QY 234 EGWSALDAIFYVITLTITIGFDGYVAG-GSDIEYLDYKPVVWFILVGLAYFAAVALSMI 292  
DB 186 EGMNIEGLIYYSFIIITIGFDGVAGVNPNSANYHALYRYFVELMIYGLAW---LSLF 241  
QY 293 GDWLRVSKKTEKEVEGFRAHAAEWNTANVTAEFKTRRLSVEIYDKFORATSIKKLSA 352  
DB 242 VNW-----KVSME-----VEVHKAIKRRR-----RKESF 267  
QY 353 ELAGNHNQELTPCRETLSVNHLTNERDV--LPPLKTSIY 391  
DB 268 E-SSPHS-----RKALQVKGSTASKDVNIFSLSKKEEY 301

RESULT 13  
US-09-431-367B-2  
; Sequence 2, Application US/09431367B  
; Patent No. 6670149  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Roy A. J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-074CP  
; CURRENT APPLICATION NUMBER: US/09/431,367B  
; CURRENT FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/259,951

```

; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-2

Query Match      20.3%; Score 427; DB 4; Length 499;
Best Local Similarity 31.1%; Pred. No. 1e-34;
Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;

Qy  54  VVLIIGATVFKALEPHSISRTTIVIQKTFISQHSVCNVSFELDELICQIVAAINAG 113
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  12  IIFALTAIGAIFEVLESPHWEAKKNYYTKLHLKEFPCLGQEGDLKILEVVSDAAGQ 71
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy  114  IILGNTSNIQSHWDLGSSFFAGTIVTTTCFGNISPRTEGKIFCIIYALLGIPLFGFL 173
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  72  VAITGNQT--FNNWNENAMIFAATVTTIGYGNVAPKTPAGRLFCVFGYGLFGVPL--C 126
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy  174  LAGVDOLGTHFGKIAKVEDTFIKNVNSQTKRIIITIIFILFGCVLFWALPAIIFKHI 233
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  127  LTWMI-SALGRFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFVGMVLVHLVIFPFVEMVT 185
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy  234  EGSALDAIYFVWITLTITIGFDGVAG-GSDIEYDFYKPVWFWILWGLAYFAAULSMI 292
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  186  EGNVIEGLYSPITISTIGFDFVAGVNPNSANYHALYRYFVELMIYILGLAW----LSLF 241
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy  293  GDMRLVISKTKBEVGSFRAHAAEWNTAETAFKETRRLRSVEIYDKFORATSIKRLSA 352
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  242  VNW-----KVSMT-----VEVHKAIKRRRR-----RKESF 267
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy  353  ELAGNNHQLTPCRTLISVNHLTNERDV--LPPLLTKESTIY 391
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  268  E-SSPHS-----RKALQVKGSTASKDVNIFSLSKKEEY 301
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 14
US-09-561-763-5
; Sequence 5, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtie, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-5

```

[illegible]

Search completed: July 13, 2005, 08:47:04  
Job time : 28.3635 secs